

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 13:12:36 ; Search time 37 Seconds

(without alignments)
257.826 Million cell updates/sec

Title: US-09-856-320A-2_COPY_53_282

Perfect score: 1263
Sequence: 1 KIKGFCECKPHSQPWQALF.....GVYTKCKYVDWIQETMKN 230

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1263	100.0	250	1 KIKB_HUMAN	Q9UBX7 homo sapien
2	739	58.5	250	1 KIK9_HUMAN	Q9UK69 homo sapien
3	689	54.6	260	1 NRPN_RAT	Q68780 rattus norv
4	686	54.3	260	1 NRPN_MOUSE	Q61955 mus musculu
5	684	54.2	236	1 KIKF_HUMAN	Q9H255 homo sapien
6	683	54.1	260	1 KIKF_HUMAN	Q60259 homo sapien
7	677.5	53.6	277	1 KIKD_HUMAN	Q9UK33 homo sapien
8	649.5	51.4	293	1 KIK5_HUMAN	Q9J337 homo sapien
9	623	49.3	251	1 KIKI_HUMAN	Q9P093 homo sapien
10	610.5	48.3	261	1 KIK1_RAT	Q9UK78 rattus norv
11	608	48.1	248	1 KIKC_HUMAN	Q9UK70 homo sapien
12	605.5	47.9	261	1 KIK7_RAT	P36373 rattus norv
13	600.5	47.5	261	1 KIK3_MOUSE	P00756 mus musculu
14	596.5	47.2	263	1 KIKR_PRANA	P32824 prionys nat
15	596	47.2	248	1 TRV3_CHICK	Q90629 gallus gall
16	593	47.0	246	1 TRV2_RAT	P00763 rattus norv
17	590.5	46.8	261	1 KIK8_RAT	P36374 rattus norv
18	590	46.7	238	1 TRV3_SALSA	P35072 sus scrofa
19	589	46.6	246	1 TRV1_RAT	P00762 rattus norv
20	586.5	46.4	259	1 KIKC_RAT	P36376 rattus norv
21	582.5	46.1	261	1 KIK2_HUMAN	P20151 homo sapien
22	582.5	46.1	261	1 KIK9_MOUSE	P15949 mus musculu
23	579	45.8	231	1 TRV2_PIG	P00761 sus scrofa
24	579	45.8	244	1 KIK6_HUMAN	Q92876 homo sapien
25	575.5	45.6	246	1 KIK_PIG	P00752 sus scrofa
26	573	45.4	246	1 TRV2_MOUSE	P00716 mus musculu
27	572.5	45.3	259	1 KIK2_RAT	P00759 rattus norv
28	571.5	45.2	261	1 KIK1_MOUSE	P15947 mus musculu
29	570	45.1	247	1 TRV2_CANFA	P06872 canis fami
30	569.5	45.1	244	1 KIK4_RAT	P36375 rattus norv
31	569.5	45.1	261	1 KIK6_MOUSE	P00755 mus musculu
32	567	44.9	262	1 KIK1_HUMAN	P06870 homo sapien
33	566	44.8	243	1 TRV1_BOVIN	P00760 bos taurus

34	563	44.6	248	1 TRV1_CHICK	Q90627 gallus gall
35	561.5	44.5	257	1 KIK1_MACFA	O07276 macaca fasc
36	561.5	44.5	261	1 KIKB_MOUSE	P15946 mus musculu
37	559	44.3	244	1 TRV2_XENLA	P70059 xenopus lae
38	559	44.3	248	1 TRV2_CHICK	Q90628 gallus gall
39	558	44.2	243	1 TRV1_XENLA	Q90628 gallus gall
40	558	44.2	247	1 TRV2_BOVIN	P19799 xenopus lae
41	556.5	44.1	261	1 KIK3_HUMAN	Q29463 bos taurus
42	555	43.9	247	1 TRV3_HUMAN	P07288 homo sapien
43	554.5	43.9	231	1 TRV3_RAT	P08426 rattus norv
44	554.5	43.9	247	1 TRV4_RAT	P35032 salmo salar
45	554	43.9	258	1 KIK1_PAPPA	P12788 rattus norv
					Q28773 papio hamad

ALIGNMENTS

RESULT 1	ID	KLKB_HUMAN	STANDARD	PRT	250 AA.
AC	Q9UBX7	075837; 09NS65;			
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Kallikrein 11 precursor (PC 3.4.21.-) (Hippocampus) (Trypsin-like protease).				
DE	Kallikrein 11 precursor (PC 3.4.21.-) (Hippocampus) (Trypsin-like protease).				
GN	KIK11 OR PRSS20 OR TLSP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Hippocampus;				
RX	MEDLINE=98438738; PubMed=9765601;				
RA	Yoshida S., Taniguchi M., Suenoto T., Oka T., He X.P., Shiosaka S.;				
RT	"cDNA cloning and expression of a novel serine protease, TLSP.";				
RL	Biochem. Biophys. Acta 1399:225-228(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 1 AND 2).				
RC	TISSUE=Hippocampus, and Prostate;				
RX	MEDLINE=20329229; PubMed=10872828;				
RA	Mitsu S., Yamada T., Okui A., Komihama K., Uemura H., Yamaguchi N.;				
RT	"A novel isoform of a kallikrein-like protease, TLSP/hippocastin, (PRSS20), is expressed in the human brain and prostate.";				
RL	Biochem. Biophys. Res. Commun. 272:205-211(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=20130117; PubMed=10662548;				
RA	Yousef G.M., Scortlas A., Diamandis E.P.;				
RT	"Genomic organization, mapping, tissue expression, and hormonal regulation of trypsin-like serine protease (TLSP/PRSS20), a new member of the human kallikrein gene family.";				
RL	Genomics 63:88-96(2000).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=20510050; PubMed=1054574;				
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.;				
RT	"Moss P., Paepker B., Wang K.;"				
RL	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";				
RN	Gene 257:119-130(2000).				
RN	[5]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RA	Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.;				
RA	Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stiliwagen S.;				
RA	Pihan H., Velasco N., Do U., Regala W., Terry A., Brown A., Gaines J.;				
RA	Dangnan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.;				
RA	Andreise T., Frankheim M., Atlix C., Amico-Keller G., Coefield J.;				
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.;				
RA	Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.;				
RA	Olsen A.S., Carrano A.V.;				
RT	"Sequence analysis of chromosome 19q13.4.";				

Aug 20

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Testis;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: POSSIBLE MULTIFUNCTIONAL PROTEASE. EFFICIENTLY CLEAVES
 CC B2-PHE-ARG-4-METHYLCOOMARYL-7-AMIDE, A KALLIKREIN SUBSTRATE, AND
 CC WEAKLY CLEAVES OTHER SUBSTRATES FOR KALLIKREIN AND TRYPSIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKIN AND PROSTATE. ISOFORM
 CC 1 IS EXPRESSED PREFERENTIALLY IN BRAIN; ISOFORM 2 IN PROSTATE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: AB012917; BAA33404.1; ALT_INIT.
 DR EMBL: AB013730; BAA8713.1; -
 DR EMBL: AB041036; BAA96797.1; -
 DR EMBL: AF164623; AAD47815.1; -
 DR EMBL: AF243527; AAG33364.1; -
 DR EMBL: AC011473; AAG32357.1; -
 DR EMBL: BC022068; AAR22068.1; -
 DR HSSP: P00763; 1DPO.
 DR MEROPS: S01.257; -
 DR Genew: HGNC:6359; KLK11.
 DR MIM: 604434; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser.protease_Try.
 DR Pfam: P00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE: PS50240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR KMW Hydrolyase; Serine protease; Glycoprotein; Signal; Zymogen;
 KM Alternative splicing.
 FT SIGNAL 1 18
 FT PROPEP 19 21
 FT CHAIN 22 250
 FT ACT_SITE 62 62
 FT ACT_SITE 110 110
 FT ACT_SITE 203 203
 FT DISULFID 28 163
 FT DISULFID 47 63
 FT DISULFID 135 237
 FT DISULFID 142 209
 FT DISULFID 174 188
 FT DISULFID 199 224
 FT CARBOHYD 99 99
 FT CARBOHYD 165 165
 FT CARBOHYD 181 181
 FT CARBOHYD 210 210
 FT VARSPLIC 1 1
 SQ SEQUENCE 250 AA; 27466 MW; 192D910BDCD7A56 CRC64;
 Query Match 100.0%; Score 1263; DR 1; Length 250;
 Best Local Similarity 100.0%; Pred. No. 7; le-109;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KLIKPECKPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLPRYIVHLGHNLOKE 60
 DB 21 KLIKPECKPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLPRYIVHLGHNLOKE 80

OY 61 EGCGRTRATESPPHGFNNSLPKDRNDIMLVKASPVSTIMWVAPRLTLSSRCVACT 120
 DB 81 EGCGRTRATESPPHGFNNSLPKDRNDIMLVKASPVSTIMWVAPRLTLSSRCVACT 140
 OY 121 SCILSGWSTSPQLRPLRLRCANITIIIEHQCENAPENITDYMVCASVDEGSDSCQ 180
 DB 141 SCILSGWSTSPQLRPLRLRCANITIIIEHQCENAPENITDYMVCASVDEGSDSCQ 200
 OY 181 GDSGGLVNCQSTLQGIISWGDPCATTRKPGVYTKVCKYVDWVIOETMKN 230
 DB 201 GDSGGLVNCQSTLQGIISWGDPCATTRKPGVYTKVCKYVDWVIOETMKN 250
 RESULT 2
 KLIK9_HUMAN
 ID KLIK9_HUMAN STANDARD; PRT; 250 AA.
 AC G9UKQ9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-13).
 GN KLIK9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20118156; PubMed=10652563;
 RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
 RT Identification of novel human kallikrein-like genes on chromosome
 RT 19q13.3-q13.4.
 RL 1993.3-913.4.
 RN [2]
 RP Anticancer Res. 19:2843-2852(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20247258; PubMed=10783266;
 RA Yousef G.M., Diamandis E.P.;
 RT "The expanded human kallikrein gene family: locus characterization and
 RT molecular cloning of a new member, KLK-13".
 RL Genomics 65:184-194(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepfer B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Iamerdin J.E., McCreedy P.M., Skowronski E., Vissanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwogen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,
 RA Dangnanan L., Erikson A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas R., Thomas G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Truong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of chromosome 19q13.4.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- TISSUE SPECIFICITY: SKIN, THYMUS, TRACHEA, CEREBELLUM AND SPINAL
 CC CORD.
 CC -----
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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CC -----
DR EMBL: AF135026; AAD26427.2; -
DR EMBL: AF243527; AAG33362.1; -
DR EMBL: AC011473; AAG23255.1; -
DR HSSP: P00763; IDPO.
DR MEROPS: S01.307; -.
DR Genew: HGNC:6370; KLK9.
DR MIM: 605504; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_try.
DR Pfam: PF00089; trypsin.1.
DR PRINTS: PR00722; CHYMOTRYPsin.
DR SMART: SM00020; TRYP_SPE.1.
DR PROSITE: PS50240; TRYPsin_DOM.1.
DR PROSITE: PS00134; TRYPsin_HIS.1.
DR PROSITE: PS00135; TRYPsin_SER.1.
KM Hydroxylase; Serine protease; Glycoprotein; signal.
FT SIGNAL 15
FT CHAIN 16 250
FT ACT_SITE 63 KALLIKREIN 9.
FT ACT_SITE 111 111 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 29 164
FT DISULFID 48 64 BY SIMILARITY.
FT DISULFID 136 238 BY SIMILARITY.
FT DISULFID 143 210 BY SIMILARITY.
FT DISULFID 175 189 BY SIMILARITY.
FT DISULFID 200 225 BY SIMILARITY.
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 250 AA; 27512 MW; F27B5245B063E98B CRC64;

Query Match 58.5%; Score 739; DB 1; Length 250;
Best Local Similarity 58.1%; Pred. No. 8,8e-61;
Matches 133; Conservative 35; Mismatches 61; Indels 0; Gaps 0;

QY 1 RIINGECKPHSPQWQALFEKTRLLCGATLIAPRLTLTAHCLKPRYVHLAGHNLQKE 60
DB 22 RAIGAEBCRPNSQPMWQAGLFLHTRLCGATLISDRWLTLTAHCKRPYLAWVLGEHHLMKW 81
QY 61 EGCEQTRTATESFPHPGPNNSLPKNDHRNDIMLVKMASPVISITAVAPRLTLSSRCVYAGT 120
DB 82 EGPEQLEFRVYDFPHPEFNNDLSANDHNDIMLIRLPQARLSPAVQPLNLSQCVSPGM 141
QY 121 SCLISGSGSTSSPOLRLPHTLRCANITITIEHOKENAYPGNITTPMVCASVQEGKXSCQ 180
DB 142 KCLISGSGAVSPKALPPLVLCANISILENKLCHMAYPGHISDMLCAGIMEGGRSCQ 201
QY 181 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDMIOETMKN 229
DB 202 GDSGGLVNCNGLAGVYSGAEPCSRPRRAVYTVCHYIDMIQEIEMEN 250

RESULT 3
NRPN_RAT STANDARD; PRT; 260 AA.
ID NRPN_RAT
AC 088780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuropeptide precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
  protease 1).
GN KLK8 OR PRSS19 OR NRPN OR BSP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-Fischer; TISSUE=Brain;
RX MEDLINE=98389725; PubMed=9722524;
RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;

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RT "Serine proteases in rodent hippocampus."
RL J. Biol. Chem. 273:23004-23011(1998).
CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
CC FIBRONECTIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-,
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: RESTRICTED TO HIPPOCAMPUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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CC -----
DR EMBL: AJ005641; CA006643.1; -
DR HSSP: Q61955; INPM.
DR MEROPS: S01.244; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_try.
DR Pfam: PF00089; trypsin.1.
DR PRINTS: PR00722; CHYMOTRYPsin.
DR SMART: SM00020; TRYP_SPE.1.
DR PROSITE: PS50240; TRYPsin_DOM.1.
DR PROSITE: PS00134; TRYPsin_HIS.1.
DR PROSITE: PS00135; TRYPsin_SER.1.
KM Hydroxylase; Serine protease; Glycoprotein; zymogen; signal.
FT SIGNAL 1 28
FT PROPEP 29 32 BY SIMILARITY.
FT CHAIN 33 260
FT ACT_SITE 73 73 NEUROPSIN.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 39 173 BY SIMILARITY.
FT DISULFID 58 74 BY SIMILARITY.
FT DISULFID 145 246 BY SIMILARITY.
FT DISULFID 152 218 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 208 233 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A0B7F5 CRC64;

Query Match 54.6%; Score 689; DB 1; Length 260;
Best Local Similarity 53.3%; Pred. No. 3,6e-56;
Matches 121; Conservative 36; Mismatches 68; Indels 2; Gaps 2;

QY 1 RIINGECKPHSPQWQALFEKTRLLCGATLIAPRLTLTAHCLKPRYVHLAGHNLQKE 60
DB 32 KILGEGCKPHSPQWQALFQGERLYVCGVLRWLTALHCKKDYSVNLGHSIQKR 91
QY 61 EGCEQTRTATESFPHPGPNNSLPKNDHRNDIMLVKMASPVISITAVAPRLTLSSRCVYAGT 120
DB 92 DEPEQEIQVARSIQHPFNSSNP-EDSHDMLIRLQNSAVLGDVPELALNCPKVG 150
QY 121 SCLISGSGSTSSPOLRLPHTLRCANITITIEHOKENAYPGNITTPMVCASVQEGKXSCQ 180
DB 151 KCLISGSGVYTSPOENFPNLTNCAEVKITYSONKERYAPGKITEGMCAG-SSNGADYQC 209
QY 181 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDMIOETM 227
DB 210 GDSGGLVNCNGLAGVITWGSDFCGKREKPGVYTKICKRTYIMIKTM 256

RESULT 4
NRPN_MOUSE STANDARD; PRT; 260 AA.
ID NRPN_MOUSE
AC 061955;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

DE Neotropin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).
GN KLK8 OR PRSS19 OR NRPN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c; TISSUE=Hippocampus;
RX MEDLINE=95348817; PubMed=7623137;
RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
RA Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
RT "Expression and activity-dependent changes of a novel limbic-serine
RT protease gene in the hippocampus.";
RL J. Neurosci. 15:5088-5097(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
RT "Cloning and assignment of mouse neotropin gene, Prss19 to chromosome
RT 7B4.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
RC STRAIN-BALB/c; TISSUE=Brain;
RX MEDLINE=98225202; PubMed=9556608;
RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
RA Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
RT "Characterization of recombinant and brain neotropin, a
RT plasticity-related serine protease.";
RL J. Biol. Chem. 273:11189-11196(1998).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
RC TISSUE=Hippocampus;
RX MEDLINE=99134351; PubMed=9933620;
RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
RA Shiosaka S., Hakoshima T.;
RT "Crystal structure of neotropin, a hippocampal protease involved in
RT kindling epileptogenesis.";
RL J. Biol. Chem. 274:4220-4224(1999).
CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
CC FIBRONECTIN.
CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-
CC -1- ENZYME REGULATION: STRONGLY INHIBITED BY DIISOPROPYL
CC FLUOROSULFATE, LEUPEPTIN AND (4-AMIDINOPHENYL)METHANESULFONYL 1-
CC FLUORIDE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE LIMBIC SYSTEM OF
CC MOUSE BRAIN AND IS LOCALIZED AT HIGHEST CONCENTRATION IN PYRAMIDAL
CC NEURONS OF THE HIPPOCAMPAL CA1-3 SUBFIELDS.
CC -1- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260.
CC -1- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC -----
DR EMBL, D30785; BAA06451.1; -
DR EMBL, AB032202; BAA92435.1; -
DR PDB, INPM: 23-MAR-99.
DR MEROPS: S01_244; -
DR MGD: MGI:892018; Kik8.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser.protease_try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYPSIN_SPEC_1.
DR PROSITE, PS50240; TRYPSIN_DOM; 1.

DR PROSITE, PS00134; TRYPSIN_HIS; 1.
DR PROSITE, PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Serine protease; Glycoprotein; Zymogen; Signal;
FT 3D-structure.
FT SIGNAL 1 28 POTENTIAL.
FT PROPEP 29 32
FT CHAIN 33 260
FT ACT_SITE 73 73 NEUROPSIN.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 39 173 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 58 74
FT DISULFID 145 246
FT DISULFID 152 218
FT DISULFID 184 198
FT DISULFID 208 233
FT CARBOHYD 110 110
SQ SEQUENCE 260 AA; 28523 MW; B556F6B37CD06E CRC64; N-LINKED (GLCNAC...) (POTENTIAL).
Query Match 54.3%; Score 686; DB 1; Length 260;
Best Local Similarity 52.8%; Pred. No. 6,7e-56;
Matches 121; Conservative 36; Mismatches 70; Indels 2; Gaps 2;
QY 1 RIIRFECRPHSQPQNALFEKTRLLCGATLLAPRHULLTRAHGLKRYIYHGLQNLQKE 60
DB 32 KILEGRECIPIHSQPQWQALFQGERLIGGLVGDWRVLAHAHCKOKYSVRLDHSLSQR 91
QY 61 EGCEQRTTSPHPGFNNSLPKNDHNDIMLVKNAAPSVITWVRPLTSSRCVTAGT 120
DB 92 DPEQELQVAGSTQHPCYNNNSN-EDHSHDIMLRQNSNGLDKKPKPQVLAHLCCKVQ 150
QY 121 SCLISGWSSTSSPOLRLPHTLRCANTITIEHOKCENAPONTIDTVWCASVQEGGKDSQ 180
DB 151 KCIISGMGTVPSPQENFPTLNCAEVKIYSQNKCEPAGFKITEGVACG-SSNGADTQ 209
QY 181 GDSGPELVNCSLOGITISNODPCATRRKPGYTYXKCYVDVQETMKN 229
DB 210 GDSGPELVNCSLOGITISNODPCATRRKPGYTYXKCYVDVQETMKN 258
RESULT 5
KLK8_HUMAN
ID KLK8_HUMAN STANDARD; PRT; 256 AA.
AC Q9H2R5; Q9H2R6; Q9H2R4; Q9H2R3; Q9H2R3; Q15358;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kallikrein 15 precursor (EC 3.4.21.-) (Aco protease).
GN KLK15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RX PubMed=11010966;
RA Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;
RT "Molecular cloning of the human kallikrein 15 gene (KLK15). Up-
RT regulation in prostate cancer.";
RL J. Biol. Chem. 276:53-61(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94289486; PubMed=8018728;
RA Dhanich M.E., Spiess M.;

RT "A novel serine proteinase-like sequence from human brain."
 RL Biochim. Biophys. Acta 1218:225-228(1994).
 CC -1- FUNCTION: Protease whose physiological substrate is not yet known.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms: 1 (shown here), 2, 3 and 4; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also
 CC expressed in the prostate, salivary, and adrenal glands and in the
 CC colon testis and kidney.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC
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 CC
 CC EMBL: AF242195; AAC09469.1; -
 CC EMBL: AF242195; AAC09470.1; -
 CC EMBL: AF242195; AAC09471.1; -
 CC EMBL: AF242195; AAC09472.1; -
 CC EMBL: AF243527; AAC33354.1; -
 CC EMBL: X75363; CA53145.1; ALT_SEQ.
 CC HSP: P00763; IDPO.
 CC MEROPS: S01.081; -
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR001254; Ser. Protease_Try.
 CC Pfam: PF00089; trypsin. 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC SMART: SM00020; TRYPSIN. 1.
 CC DR PROSITE: PS50240; TRYPSIN_DOM. 1.
 CC PROSITE: PS00134; TRYPSIN_HIS. 1.
 CC DR PROSITE: PS00135; TRYPSIN_SER; FALSE NEG.
 CC KM Hydrolyase: Serine protease; Glycoprotein; signal; zymogen;
 CC KM Alternative splicing.
 CC FT SIGNAL: 1
 CC FT PROPEP: 17
 CC FT CHAIN: 22
 CC FT ACT_SITE: 62
 CC FT ACT_SITE: 106
 CC FT ACT_SITE: 209
 CC FT CARBOHYD: 171
 CC FT CARBOHYD: 232
 CC FT VARSPLIC: 122
 CC FT VARSPLIC: 122
 CC FT VARSPLIC: 161
 CC FT VARSPLIC: 162
 CC FT CONFLICT: 147
 CC SQ SEQUENCE: 256 AA; 28087 MW; B5EBF8D6022786B5 CRC64;
 Query Match 54.2%; Score 684; DB 1; Length 256;
 Best Local Similarity 51.7%; Pred. No. 1e-55;
 Matches 12; Conservative 37; Mismatches 65; Indels 14; Gaps 3;

RESULT 6
 K18_HUMAN STANDARD: PRT; 260 AA.
 ID K18_HUMAN
 AC 060259; Q9U047; Q9HCB3; Q9U1L9;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuropilin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine
 DE protease TADG-14) (Tumor-associated differentially expressed gene-14
 DE protein).
 GN K18 OR PRS19 OR TADG4 OR NRPN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hippocampus;
 RX MEDLINE=98372070; PubMed=9714609;
 RA Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
 RT "Sequence analysis and expression of human neuropilin cDNA and gene."
 RT Gene 213:9-16(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=99203457; PubMed=10102990;
 RA Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
 RT "A novel form of human neuropilin, a brain-related serine protease, is
 RT generated by alternative splicing and is expressed preferentially in
 RT human adult brain."
 RT Eur. J. Biochem. 260:627-634(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Ovary;
 RX MEDLINE=99413504; PubMed=10485494;
 RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
 RA O'Brien T.J.;
 RT "Cloning of tumor-associated differentially expressed gene-14, a novel
 RT serine protease overexpressed by ovarian carcinoma."
 RT Cancer Res. 59:4435-4439(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Gan L., Gellinas R., Gown A.M., Moss P., Smith R., Wang K.;
 RT "Molecular cloning and characterization of a novel serine protease,
 RT ovasin, a potential molecular marker for ovarian carcinomas."
 RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaty J.,
 RA Moss P., Paepfer B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region."
 RT Gene 257:119-130(2000).
 RN [6]
 RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).
 RA Lemerding J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Pan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,
 RA Danganan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Duarte S., Lucas S., Bruce R., Attix C., Amico-Keller G., Coffield J.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of chromosome 19q13.4."
 RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
 CC HIPPOCAMPAL PLASTICITY.
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE

CC PANCREAS WHILE ISOFORM 2 IS EXPRESSED IN ADULT BRAIN AND
 CC HIPPOCAMPUS. BOTH FORMS ARE ALSO FOUND IN FETAL BRAIN AND
 CC PLACENTA. NOT DETECTED IN KIDNEY, SPLEEN, LIVER AND LUNG.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: AB009849; BAA28673.1; -
 DR EMBL: AB012761; BAA28676.1; -
 DR EMBL: AB010780; BAA88684.1; -
 DR EMBL: AB008390; BAA82665.1; -
 DR EMBL: AB008927; BAA82666.1; -
 DR EMBL: AF055982; AAD56050.1; -
 DR EMBL: AF095742; AAD25979.1; -
 DR EMBL: AF095743; AAD29574.1; -
 DR EMBL: AF243527; AAG33361.1; -
 DR EMBL: AC011473; AAG23254.1; -
 DR HSSP: 061955; 1NPM.
 DR MEROPS: S01.244; -
 DR Genev: HGNC:6369; KLR8.
 DR MIM: 605644; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser.protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPsin.
 DR SMART: SM00020; TRYP_Spc.1.
 DR PROSITE: PS00240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR Hydrolase: Serine protease; Glycoprotein; zymogen; signal;
 KM
 FT Alternative splicing 28
 FT SIGNAL 1
 FT PROPEP 29 32
 FT CHAIN 33 260
 FT ACT_SITE 73 73
 FT ACT_SITE 120 120
 FT ACT_SITE 212 212
 FT DISULFID 39 173
 FT DISULFID 58 74
 FT DISULFID 145 246
 FT DISULFID 152 218
 FT DISULFID 184 198
 FT DISULFID 208 233
 FT CARBOHYD 110 110
 FT VARSPLIC 23 23
 SQ SEQUENCE 260 AA; 28048 MW; EPA39E5B8C83E660 CRC64;
 Query Match 54.1%; Score 683; DB 1; Length 260;
 Best Local Similarity 51.6%; Pred. No. 1.3e-55;
 Matches 116; Conservative 43; Mismatches 64; Indels 2; Gaps 2;

RESULT 7
 ID KLRD_HUMAN STANDARD; PRT; 277 AA.
 AC Q9UKR3; Q9Y433;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)
 DE (KLR-L4).
 GN KLR13 OR KLR14
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20229789; PubMed-10766816;
 RA Yousef G.M., Chang A., Diamandis E.P.;
 RT Identification and characterization of KLR-L4, a new kallikrein-like
 RT gene that appears to be down-regulated in breast cancer tissues.;
 RL J. Biol. Chem. 275:11891-11898(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
 RA Pan H., Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J.,
 RA Dargatzis L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andeise T., Trankeheim M., Atlix C., Amico-Keller G., Coelield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Tong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RT *Sequence analysis of chromosome 19q13.4.*
 RL Submitted (Oct-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-180 FROM N.A.
 RC TISSUE=uterus;
 RA Ansoorge W., Wilkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, BREAST, TESTIS AND
 CC SALIVARY GLAND.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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 CC -----
 DR EMBL: AF135024; AAD26425.2; -
 DR EMBL: AC011473; AAG23259.1; -
 DR EMBL: AL050220; CAB43320.1; ALT_INIT.
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.306; -
 DR Genev: HGNC:6361; KLR13.
 DR MIM: 605505; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser.protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPsin.
 DR SMART: SM00020; TRYP_Spc.1.
 DR PROSITE: PS00240; TRYPsin_DOM; 1.
 DR PROSITE: PS00134; TRYPsin_HIS; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 DR Hydrolase; Serine protease; Glycoprotein; signal.
 FT SIGNAL 1
 FT CHAIN 17 277
 FT ACT_SITE 76 76
 FT ACT_SITE 124 124
 FT ACT_SITE 124 124
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).

```

FT ACT_SITE 218 218 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 42 178 BY SIMILARITY.
FT DISULFID 61 77 BY SIMILARITY.
FT DISULFID 157 224 BY SIMILARITY.
FT DISULFID 189 203 BY SIMILARITY.
FT DISULFID 214 239 BY SIMILARITY.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 170 180 VNYPKLOCAN -> GMPHPRWEAP (IN REF. 3).
SQ SEQUENCE 277 AA; 30570 MW; BA8A9EBDCFB5D542 CRC64;

Query Match 53.6%; Score 677.5; DB 1; Length 277;
Best Local Similarity 53.3%; Pred. No. 4.3e-55;
Matches 120; Conservative 41; Mismatches 63; Indels 1; Gaps 1;

QY 5 GFECKPHSOPMAALFEKTRLLCGATLLAPRWLLTAHCLPKRYIVHLGQHNLOKESGE 64
   1: ||||| ||||| : ||||| : ||||| ||||| : ||||| : |||||
Db 39 GYCFPHSQPQMAALLVOGRLLCGVLYHPKRVLTAAHCLKEGLKYLGLKHALGRLEAGE 98
   1: ||||| ||||| : ||||| : ||||| ||||| : ||||| : |||||
QY 65 QTRATESPFPHPGNNSLPNKDRNDIMLVKMASPVITMAVRPLTUS-SKCVTAGTSC 123
   1: ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 99 QREVVHISIPPEYRSPRTHLNDHDMLELQSPVOLTGYITPLSHNNRLTPGTTCR 158
   1: ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 124 ISGSGTSSPOLRLPHLRCANITLIEHCKCENAYPGNIIDPTMCAVQEGKSCGDS 183
   1: ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 159 VSGGTTSPQVNPYKTLQCANIQLRSEDECRQYYPKRTIDNMCACTKEGKSCGDS 218
   1: ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 184 GGPLVNCNOSLOGIISMGODPCATRRKPGYTVKCYVDWIOETFK 228
   1: ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 219 GGPLVNCNRLXGIVSMGDFPGQDPGRGVTVRSRYVLMIREITR 263
   1: ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 8
KLK5_HUMAN STANDARD; PRT; 293 AA.
AC G9Y337; G9H8G8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)
GN Kallikrein-like protein 2 (KLK-12).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stratum corneum;
RA Brattsand M., Egelrud T.;
RT "Purification, molecular cloning, and expression of a human stratum
RT corneum trypsin-like serine protease with possible function in
RT desquamation.", 19:2843-2852(1999).
RL J. Biol. Chem. 274:30033-30040(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13-q13.4.", 19:2843-2852(1999).
RL Anticancer Res. 19:2843-2852(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepert B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.",
RL Gene 257:119-130(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;

```

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RA Strausberg R.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY BE INVOLVED IN DESQUAMATION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKIN, BREAST, BRAIN AND TESTIS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC -----
DR EMBL: AF168768; AAF03101.1; -.
DR EMBL: AF135028; AAD26429.1; -.
DR EMBL: AF243527; AAG33358.1; -.
DR EMBL: BC008036; AAR08036.1; -.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.017; -.
DR Genes: HGNC:6366; KLK5.
DR MIM: 605643; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PSS00240; TRYP_SIN_DOM; 1.
DR PROSITE: PS00134; TRYP_SIN_HIS; 1.
DR PROSITE: PS00135; TRYP_SIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 293
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 153 153 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 245 245 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 73 206 BY SIMILARITY.
FT DISULFID 93 109 BY SIMILARITY.
FT DISULFID 178 279 BY SIMILARITY.
FT DISULFID 185 251 BY SIMILARITY.
FT DISULFID 217 231 BY SIMILARITY.
FT DISULFID 241 266 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 25 56 MISSING (IN REF. 3).
SQ SEQUENCE 293 AA; 32020 MW; D92C92F5609E5946 CRC64;

Query Match 51.4%; Score 649.5; DB 1; Length 293;
Best Local Similarity 50.9%; Pred. No. 1.7e-52;
Matches 118; Conservative 40; Mismatches 67; Indels 7; Gaps 4;

QY 1 RIIFGFECKPHSOPMAALFEKTRLLCGATLLAPRWLLTAHCLPKRYIVHLGQHNLOK 59
   1: ||||| ||||| : ||||| : ||||| ||||| : ||||| : |||||
Db 66 RIIFGSDCDHNTQPMQAAALLRPWLYCGAVLYHPWLLTAHCKRKYVERRLGHTSLP 125
   1: ||||| ||||| : ||||| : ||||| ||||| : ||||| : |||||
QY 60 -EESCEQTRATESPFPHPGNNSLPNKDRNDIMLVKMASPVITMAVRPLTUSKCVTA 118
   1: ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 126 VYESGQDMFOGVKSIPHGYG---HPGSHNDIMLILNRRIRPTKDVPRINWSSHCPSA 181
   1: ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 119 GTSCLISGSGTSSPOLRLPHLRCANITLIEHCKCENAYPGNIIDPTMCAVQEGKDS 178
   1: ||||| ||||| : ||||| : ||||| ||||| : ||||| : |||||
Db 182 GTKVLVSGMGTTSPQVNPYKRVLYLQCLNIIVLSQKRCDAVPRQIDPTMFCAG-DKAGRDS 240
   1: ||||| ||||| : ||||| : ||||| ||||| : ||||| : |||||
QY 179 CGGDSGGLVNCNOSLOGIISMGODPCATRRKPGYTVKCYVDWIOETFK 230
   1: ||||| ||||| : ||||| : ||||| ||||| : ||||| : |||||
Db 241 CGGDSGGLVNCNOSLOGIISMGODPCARPRNPGYTVMLCKFTKWIQETIQAN 292
   1: ||||| ||||| : ||||| : ||||| ||||| : ||||| : |||||

RESULT 9
KLK5_HUMAN

```

ID KLKE_HUMAN STANDARD; PRT; 251 AA.
AC Q9P0G3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6) (KIK-16).
GN KLIK14 OR KLIK16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yousef G.M., Diamandis E.P.;
RT "Molecular characterization, mapping, and tissue expression of KLIK16, a hormonally regulated kallikrein-like gene."
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RA Hooper J.D., Bul L.T., Rae F.K., Harvey T.J., Myers S.A., Ashworth L.K., Clements J.A.;
RT "Identification and characterization of KLIK14, a novel kallikrein serine protease gene located on human chromosome 19q13.4 and expressed in prostate and skeletal muscle."
RL Genomics 73:117-122(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V., Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S., Phan H., Velasco N., Do L.T., Regala W., Terry A., Brower A., Barnes J., Danganan L., Erlar A., Christensen K., Georgescu A., Avila J., Liu S., Andeise T., Trankheim M., Atlix C., Amico-Keller G., Coesfield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.S., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4."
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP TISSUE SPECIFICITY.
RA MEDLINE=20545474; PubMed=10969073;
RA Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K., Clements J.A.;
RT "Tissue-specific expression patterns and fine mapping of the human Kallikrein (KIK) locus on proximal 19q13.4."
RL J. Biol. Chem. 275:37397-37406(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, BONE MARROW AND FETAL LIVER. ALSO EXPRESSED IN LIVER, PANCREAS, PETAL SPLEEN, PROSTATE AND SKELETAL MUSCLE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC -----
DR EMBL: AF161221; AAD50773.2; -
DR EMBL: AF283669; AAK48523.1; -
DR EMBL: AF283670; AAK48524.1; -
DR EMBL: AC011473; AAG3260.1; -
DR HSSP: P00763; IDPO.
DR MEROPS: S01.029; -
DR Genew: HGNC:6362; KLIK14.
DR MIM: 606135; -
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin.1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_Spc; 1.

DR PROSITE: P550240; TRYPSIN_DOM; 1.
DR PROSITE: P500134; TRYPSIN_HIS; 1.
DR PROSITE: P500135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal; zymogen.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 251
FT ACT_SITE 67 67
FT ACT_SITE 111 111
FT ACT_SITE 204 204
FT DISULFID 31 164
FT DISULFID 52 68
FT DISULFID 143 210
FT DISULFID 175 189
FT DISULFID 200 225
SO SEQUENCE 251 AA; 27452 MW; 9087953BAFA7D25 CRC64;
Query Match 49.3%; Score 623; DB 1; Length 251;
Best Local Similarity 48.9%; Pred. No. 3.9e-50;
Matches 113; Conservative 38; Mismatches 74; Indels 6; Gaps 2;
QY 1 RIKGFECKPHSOPMOALF--EKTRLCGATLAPRMILTAHCLKPRYIHLGQHNQ 58
DB 24 KIIGGHTCTRSSQPMQALLAGPRRFLCGGALISQWYITAAHGRPILOYALGKHNR 83
QY 59 KEKGCEQRTFATESPPHGFENNSLPKNDHNDIMLVKMASPVSTWAVRPLTSSRCVYA 118
DB 84 RWEATQVLRVRYQVTHPNVY----SRTHNDMLLQGPARGRAVPIEVTAQACASP 139
QY 119 GRSCLISGSGTSSPOLRLPHLRKANITIERKQCEANYPGNTIDYWCASVQEGKDS 178
DB 140 GTSICRSGTIGTSSPLARPAASLCVNNISPEVCQKYPRTIIPGMVACAGVPGKDS 199
QY 179 CGDSSGPRVYCNQSLGSIISMGODPCAIRKPGVYTKVCKYDIOETKN 229
DB 200 CGDSSGPRVYCNQSLGSIISMGODPCAIRKPGVYTKVCKYDIOETKN 250
RESULT 10
KLIK1_RAT
ID KLIK1_RAT STANDARD; PRT; 261 AA.
AC P00758;
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glandular kallikrein, pancreatic 1 precursor (EC 3.4.21.35) (Tissue kallikrein) (PS kallikrein) (RCK-1).
GN KLIK OR KIK-1.
OS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=83117659; PubMed=6961406;
RA Swift G.H., Dagorn J.-C., Ashley P.L., Cummings S.W., McDonald R.J.;
RT "Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of the encoded preproenzyme."
RL Proc. Natl. Acad. Sci. U.S.A. 79:7263-7267(1982).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Submaxillary gland;
RC MEDLINE=86051477; PubMed=2998455;
RA Ashley P.L., MacDonald R.J.;
RT "Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of four distinct types including tonin."
RL Biochemistry 24:4512-4520(1985).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Kidney;
RC MEDLINE=89327211; PubMed=2753879;
RA Inoue H., Fukui K., Miyake Y.;
RT "Identification and structure of the rat true tissue kallikrein gene

RT expressed in the kidney." ;
 RL J. Biochem. 105:834-840(1989).
 RN (4)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=69214217; PubMed=2708383;
 RA Mines D.R., Brady J.M., Pitchett D.B., Roberts J.L., Macdonald R.J.;
 RT "Organization and expression of the rat kallikrein gene family." ;
 RL J. Biol. Chem. 264:7653-7662(1989).
 RN (5)
 RP SEQUENCE OF 48-261 FROM N.A.
 RX MEDLINE=86131678; PubMed=3004582;
 RA Gerald W.L., Chao J., Chao L.;
 RT "Immunological identification of rat tissue kallikrein cDNA and
 characterization of the kallikrein gene family." ;
 RL Biochem. Biophys. Acta 866:1-14(1986).
 CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
 CC IN KININOGEN TO RELEASE LYS-BRADYKININ.
 CC -1- CATALYTIC ACTIVITY: preferential cleavage of Arg-I-Xaa bonds in
 CC small molecule substrates. Highly selective action to release
 CC kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
 CC Met-I-Xaa or Leu-I-Xaa.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: J00758; ; NOT_ANNOTATED_CDS.
 DR EMBL: M11563; AAA41464.1; ALT_INIT.
 DR EMBL: M23876; AAA41462.1; -.
 DR EMBL: M23874; AAA41462.1; JOINED.
 DR EMBL: M23875; AAA41462.1; JOINED.
 DR EMBL: D00448; BAA00346.1; ALT_INIT.
 DR EMBL: D00446; BAA00346.1; JOINED.
 DR EMBL: D00447; BAA00346.1; JOINED.
 DR EMBL: X03560; CAA27247.1; -.
 DR PIR: A00944; KORTP.
 DR PIR: A23863; A23863.
 DR PIR: JX0073; JX0073.
 DR PIR: A33359; A33359.
 DR HSSP: P00757; ISGF.
 DR MEROPS: S01.405; -.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser.protease_Try.
 DR Pfam: PF00089; trypsin.1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPC.1.
 DR PROSITE: PS50240; TRYPsin.DOM.1.
 DR PROSITE: PS00134; TRYPsin.HIS.1.
 DR PROSITE: PS00135; TRYPsin_SER.1.
 KW Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;
 KW Signal.
 FT SIGNAL 1 18 PROBABLE.
 FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
 FT CHAIN 25 261 GLANDULAR KALLIKREIN 1.
 FT CHAIN 111 111 CHAIN 1.
 FT CHAIN 112 261 CHAIN 2.
 FT ACT_SITE 65 65 CHARGE RELAY SYSTEM.
 FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.
 FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
 FT DISULFID 31 173 BY SIMILARITY.
 FT DISULFID 50 66 BY SIMILARITY.
 FT DISULFID 152 219 BY SIMILARITY.
 FT DISULFID 184 198 BY SIMILARITY.
 FT DISULFID 209 234 BY SIMILARITY.
 FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (PROBABLE).
 SQ SEQUENCE 261 AA; 28852 MW; F2F99C0227A7882B CRC64;
 Query Match 48.3%; Score 610.5; DB 1; Length 261;

Best Local Similarity 45.6%; Pred. No. 5.7e-49;
 Matches 108; Conservative 43; Mismatches 79; Indels 7; Gaps 1;
 QY 1 RIIFGECKPSPQWQALFEKTRILGATLIARWLLTAACHKPRIVLHGOHNILOKE 60
 Db 24 RVAGGYNENMSQPMQVAVYFEGELCGVILIDSWVITAAHCATNDVQWGLGRNLYED 83
 QY 61 EGCEQRTATESPPHGFENSL-----PKKDRNDIMLVKMSPVSTVAVRPLTSS 113
 Db 84 EPFAQHRIVSQSPHPGFENQDILNNHTRQPDGDDYSNDMLLHLSOPADITGVKVIDPI 143
 QY 114 RCYVATGSLISGSGSSPPQLRPHLRCAHNTIIEHCKENAVPGNITPTWCASVQE 173
 Db 144 EEPKVGSTCLASGWSITPDGLEISDDLCVNDILSNKCVFAHKEEVTMLMCAEMD 203
 QY 174 GKRSCGDSGPVYVQMSLOGIISGODPCATRRKPGVYTKCKYVDVIOETKKN 230
 Db 204 GGRDTCKGDSGPLICNGVILQITISWGFNCGEKKRKYITKLKFTPMIKEVKEN 260
 RESULT 11
 K1KC_HUMAN STANDARD; PRT; 248 AA.
 AC 09UKR0; 09UKR1; Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)
 DE (K1K1-15)
 GN K1K12 OR K1K15.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20118156; PubMed=10652563;
 RA Yousif G.M., Luo L.-Y., Diamandis E.P.;
 RT "Identification of novel human kallikrein-like genes on chromosome
 RT 19q13.3-q13.4." ;
 RL Anticancer Res. 19:2843-2852(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Yousif G.M., Magklara A., Scorilas A., Diamandis E.P.;
 RT "Cloning of new alternatively spliced forms of the kallikrein-like
 RT gene 5 (K1K1-15)." ;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuall J.,
 RA Moss P., Paepfer B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region." ;
 RL Gene 257:119-130(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Iamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez W., Stllwagen S.,
 RA Phan H., Velasco N., Do H., Regala W., Terry A., Brower A., Gaines J.,
 RA Dangnan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Frankel M., Altix C., Amico-Keller G., Coeffield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carraro A.V.;
 RT "Sequence analysis of chromosome 19q13.4." ;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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QY 1 RIIFGECKPHSOPWQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLCQHNLOKE 60
 DB 24 RIVIGFCEKSNKSOPOWALVFTKGLIDPSWVITTAHCSNNYOVWLCGRNNLLED 83
 QY 61 EGCQOTATSPHPHCPGPNNSL-----PKDHRNDIMLVKMASPVSTMAVRLTLSS 113
 DB 84 EPPAQHFLVSGSEPHPYKPKPLMRNTRKPEDDHSNDMLMLHLSQPADITDGVVIDPPT 143
 QY 114 RCYVAGTSCILSGWSTSSPOLRLPHLRCAANTIIEHOKCENAYPCNITDVMCASVOE 173
 DB 144 EEPVAGSTCLASGWSGTRKPLMERFPDQLQCNHILSNCKIKRYKRYVDMLCAGELE 203
 QY 174 GKDSCGDSGGPLVNCQSLQGIISWGODPCATRRKPGVYTKVCKYDWMIOETMKN 230
 DB 204 GAKDTCTGDSGGLCDGVLOGITSMGSCVCAKTNMPATYTKLKFTSMWIKRYMKN 260
 RESULT 13
 KLR3_MOUSE STANDARD; PRT; 261 AA.
 ID KLR3_MOUSE
 AC P00756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Glandular kallikrein K3 precursor (EC 3.4.21.35) (Tissue kallikrein)
 DE (mGK-3) (7S nerve growth factor gamma chain) (Gamma-NGF).
 GN KLR3 OR KLR-3 OR NGFG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85076169; PubMed=6548955;
 RA Ullrich A., Gray A., Wood W.I., Hayflick J., Seeburg P.H.;
 RT "Isolation of a cDNA clone coding for the gamma-subunit of mouse
 RT nerve growth factor using a high-stringency selection procedure.";
 RT DNA 3:387-392(1984).
 RL [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=85257431; PubMed=3848399;
 RA Evans B.A., Richards R.I.;
 RT "Genes for the alpha and gamma subunits of mouse nerve growth factor
 RT are contiguous.";
 RT EMBO J. 4:133-138(1985).
 RL [3]
 RP SEQUENCE OF 25-261.
 RX MEDLINE=81264363; PubMed=7263706;
 RA Thomas R.A., Beglan N.C., Bradshaw R.A.;
 RT "The amino acid sequence of the gamma-subunit of mouse submaxillary
 RT gland 7 S nerve growth factor.";
 RT J. Biol. Chem. 256:9156-9166(1981).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
 RC STRAIN-Sites Webster; TISSUE-Submaxillary gland;
 RX MEDLINE=98035451; PubMed=9351801;
 RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;
 RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
 RT four binding proteins.";
 RT Structure 5:1275-1285(1997).
 RL [-]
 CC FUNCTION: 7S NGF ALPHA CHAIN STABILIZES THE 7S COMPLEX. THE BETA
 CC DIMER PROMOTES NEURITE GROWTH. THE GAMMA CHAIN IS AN ANGININE-
 CC SPECIFIC PROTEASE; IT MAY ALSO HAVE PLASMINOGEN ACTIVATOR
 CC ACTIVITY, AS WELL AS MITOGENIC ACTIVITY FOR CHICK EMBRYO
 CC FIBROBLASTS.
 CC [-]
 CC CATALYTIC ACTIVITY: Preferential cleavage of Arg-I-Xaa bonds in
 CC small molecule substrates. Highly selective action to release
 CC kallidin (Lysyl-Bradykinin) from kinogen involves hydrolysis of
 CC Met-I-Xaa or Leu-I-Xaa.
 CC [-]
 CC SUBUNIT: 7S NERVE GROWTH FACTOR IS COMPOSED OF TWO ALPHA CHAINS,
 CC A BETA DIMER COMPOSED OF IDENTICAL CHAINS, AND TWO GAMMA CHAINS.
 CC [-]
 CC MISCELLANEOUS: THIS PRECURSOR IS CLEAVED INTO SEGMENTS TO PRODUCE
 CC THE ACTIVE FORM OF THE GAMMA CHAIN, WHICH OCCURS NATURALLY AS

CC COMBINATIONS OF EITHER TWO OR THREE SEGMENTS HELD TOGETHER BY
 CC DISULFIDE BONDS: B1 + A OR B1 + C + B2.
 CC [-]
 CC SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X01389; CAA25645.1; -
 CC EMBL: X01798; CAA25928.1; -
 CC EMBL: X01799; CAA25930.1; -
 CC PIR: A00942; NCMG.
 CC PDB: 1SGF; 27-MAY-98.
 CC MEROPS: S01.170; -
 CC MGD: MGI:97322; Ngfg.
 CC InterPro: IPR001314; Chymotrypsin.
 CC InterPro: IPR001254; Ser_protease_Try.
 CC Pfam: PF00089; trypsin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC SMART: SM00020; TRYPSIN_DOM; 1.
 CC PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC KMW: Hydrolyase; Serine protease; Glycoprotein; Multigene family; Zymogen;
 CC Signal; Growth factor; 3D-structure.
 CC FT SIGNAL 1 18 PROBABLE.
 CC FT PROPEP 19 24 ACTIVATION PEPTIDE.
 CC FT CHAIN 25 261 GLANDULAR KALLIKREIN K3.
 CC FT CHAIN 25 107 NERVE GROWTH FACTOR GAMMA CHAIN 1.
 CC FT CHAIN 112 261 NERVE GROWTH FACTOR GAMMA CHAIN 2.
 CC FT ACT_SITE 65 65 CHARGE RELAY SYSTEM.
 CC FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.
 CC FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
 CC FT DISULFID 31 173
 CC FT DISULFID 50 66
 CC FT DISULFID 152 219
 CC FT DISULFID 184 198
 CC FT DISULFID 209 234
 CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .).
 CC FT DOMAIN 25 107 SEGMENT B1.
 CC FT DOMAIN 112 261 SEGMENT A.
 CC FT DOMAIN 112 164 SEGMENT C.
 CC FT DOMAIN 165 261 SEGMENT B2.
 CC FT CONFLICT 108 111 MISSING (IN REF. 2).
 CC SQ SEQUENCE 261 AA; 28998 MW; 4870748E174AF7C8 CRC64;
 CC
 CC Query Match 47.5%; Score 600.5; DB 1; Length 261;
 CC Best local Similarity 44.7%; Pred. No. 4.7e-48;
 CC Matches 106; Conservative 46; Mismatches 78; Indels 7; Gaps 1;
 CC
 CC QY 1 RIIFGECKPHSOPWQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLCQHNLOKE 60
 DB 24 RIVIGFCEKSNKSOPOWALVFTKGLIDPSWVITTAHCSNNYOVWLCGRNNLLED 83
 QY 61 EGCQOTATSPHPHCPGPNNSL-----PKDHRNDIMLVKMASPVSTMAVRLTLSS 113
 DB 84 EPPAQHFLVSGSEPHPYKPKPLMRNTRKPEDDHSNDMLMLHLSQPADITDGVVIDPPT 143
 QY 114 RCYVAGTSCILSGWSTSSPOLRLPHLRCAANTIIEHOKCENAYPCNITDVMCASVOE 173
 DB 144 EEPVAGSTCLASGWSGTRKPLMERFPDQLQCNHILSNCKIKRYKRYVDMLCAGELE 203
 QY 174 GKDSCGDSGGPLVNCQSLQGIISWGODPCATRRKPGVYTKVCKYDWMIOETMKN 230
 DB 204 GAKDTCTGDSGGLCDGVLOGITSMGSCVCAKTNMPATYTKLKFTSMWIKRYMKN 260
 RESULT 14
 KLR3_PRANA

ID KLRK_PRANA STANDARD; PRT: 263 AA.
AC P32824;
DT 01-OCT-1993 (Rel. 27, Created)
DR 01-OCT-1993 (Rel. 27, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glandular kallikrein, renal precursor (EC 3.4.21.35) (Tissue kallikrein).
OS Prionys natalensis (African soft-furred rat) (Mastomys natalensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mastomys.
OX NCBI_TaxID=10112;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=94226702; PubMed=7909667;
RA Farnesstock M.;
RT "Characterization of kallikrein cDNAs from the African rodent Mastomys".
RL DNA Cell Biol. 13:293-300(1994).
CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS IN KININOGEN TO RELEASE LYS-BRADYKININ.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-I-Xaa bonds in small molecule substrates. Highly selective action to release kallidin (lysyl bradykinin) from kininogen involves hydrolysis of Met-I-Xaa or Leu-I-Xaa.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL: X17352; CA35232.1; -
DR DR PIR: S15686; S15686.
DR HSSP: P00757; 1SGF.
DR MEROPS: S01.160; -
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR SMART: SM00020; tryp-Spc: 1.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Serine protease; Glycoprotein; Multigene family; Zymogen.
KM Signal.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 263 GLANDULAR KALLIKREIN, RENAL.
FT ACT_SITE 65 65 CHARGE RELAY SYSTEM.
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM.
FT ACT_SITE 215 215 CHARGE RELAY SYSTEM.
FT DISULFID 31 175 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 153 221 BY SIMILARITY.
FT DISULFID 186 200 BY SIMILARITY.
FT DISULFID 211 236 BY SIMILARITY.
FT CAROHND 102 102 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 263 AA; 29130 MW; A8EB023B800337D5 CRC64;

Query Match 47.2%; Score 596.5; DB 1; Length 263;
Best Local Similarity 44.8%; Pred. No. 1,1e-47;
Matches 107; Conservative 44; Mismatches 79; Indels 9; Gaps 2;

OY 1 RIIFGEFCKPHSQPQWALFEKTRLLCATLAPRLTLTAACLPKRYVHVGSHLOKE 60
DB 24 RIIFGEFCKPHSQPQWALFEKTRLLCATLAPRLTLTAACLPKRYVHVGSHLOKE 60
OY 61 ECGEOTRTATESFPHGPFNNSLPNKDH-----RNDIMLVKMASPVSTWAVRPLTJS 112

DB 84 EPSAQHQLSKALPHGPFNNSLPNKDH-----RNDIMLVKMASPVSTWAVRPLTJS 143
OY 113 SRCVTAGTSCILSGMGSTSPOLRLPHLRCANITIEHOCENAYPCNITDVMCASV 171
DB 144 TEEPTVGSRCILSGMGSTSPOLRLPHLRCANITIEHOCENAYPCNITDVMCASV 203
OY 172 OEGKDSGCGDSCGPGVPLVCSLOGITISMGODPCATRRKGVYTKVYVDMIOETMKN 230
DB 204 MGGKDTGVGDSGPGVPLVCSLOGITISMGODPCATRRKGVYTKVYVDMIOETMKN 262

RESULT 15
TRY3_CHICK
ID TRY3_CHICK STANDARD; PRT: 248 AA.
AC Q90629;
DT 01-NOV-1997 (Rel. 35, Created)
DR 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Trypsin II-p29 precursor (EC 3.4.21.4).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=pancreas;
RX MEDLINE=95251611; PubMed=7733885;
RA Wang K., Gan L., Lee I., Hood L.E.;
RT Isolation and characterization of the chicken trypsinogen gene family.";
RL Biochem. J. 307:471-479(1995).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-I-Xaa, Lys-I-Xaa.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE PANCREAS WHILE LOWER LEVELS ARE FOUND IN THE LIVER, SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL: U15157; AAA79914.1; -
DR DR HSSP: P00763; IDPO.
DR MEROPS: S01.151; -
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR SMART: SM00020; tryp-Spc: 1.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Serine protease; Digestion; Pancreas; Zymogen; Signal; Multigene family.
KM Signal.
FT SIGNAL 1 16 BY SIMILARITY.
FT PROPEP 17 25 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 26 248 TRYPSIN II-p29.
FT ACT_SITE 65 65 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 109 109 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 202 202 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 32 162 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 134 235 BY SIMILARITY.
FT DISULFID 141 208 BY SIMILARITY.
FT DISULFID 173 187 BY SIMILARITY.
FT DISULFID 196 222 BY SIMILARITY.
FT SITE 196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2002, 14:23:37 ; Search time 69 Seconds

(without alignments)
1022.256 Million cell updates/sec

Title: US-09-856-320a-2_COPY_53_282

Perfect score: 1263

Sequence: 1 RIKKGECKPHSQPQWQALF.....GYTVKCKYVWIDQETMKNK 230

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Xgapop 10.0	Xgapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool/US09856320/runat.23122002.113712.22728/app_query.fasta_1.391
-DB=Issued_Patents.NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -IOPCtl=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdt
-LIST=45 -DOCLALIG=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIG=15
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-NO.XLPXY -NO.MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents.NA.*
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2: /cgn2.6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2.6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2.6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2.6/ptodata/2/ina/PTCUS.COMB.seq.*
6: /cgn2.6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1263	100.0	1192	4	US-08-944-483-8
2	1263	100.0	1314	3	US-09-025-059-2
3	1251	99.0	1166	4	US-08-944-483-7
4	1221.5	96.7	1052	4	US-09-386-642-10
5	1218	96.4	833	2	US-08-790-137-2
6	916.5	72.6	618	4	US-09-280-116-3
7	683	54.1	944	3	US-09-070-526-1
8	675	53.4	994	4	US-09-008-271A-19
9	673.5	53.3	1049	4	US-09-386-642-9
10	636.5	50.4	1476	2	US-08-874-874-2
11	636.5	50.4	1476	4	US-09-210-084-2
12	634.5	50.2	1364	4	US-09-280-116-20

13	582.5	46.1	766	3	US-08-768-859A-9	Sequence 9, Appl1
14	582.5	46.1	766	3	US-08-767-820A-9	Sequence 9, Appl1
15	582.5	46.1	766	3	US-08-622-046B-17	Sequence 17, Appl1
16	582.5	46.1	766	4	US-09-100-264-6	Sequence 6, Appl1
17	582.5	46.1	822	4	US-09-100-264-8	Sequence 8, Appl1
18	582.5	46.1	832	3	US-08-768-859A-5	Sequence 5, Appl1
19	582.5	46.1	832	3	US-08-767-820A-5	Sequence 5, Appl1
20	582.5	46.1	832	3	US-08-622-046B-15	Sequence 15, Appl1
21	582.5	46.1	1341	4	US-08-983-075D-6	Sequence 6, Appl1
22	582.5	46.1	1358	4	US-08-983-075D-8	Sequence 8, Appl1
23	579.5	45.9	766	3	US-08-622-046B-6	Sequence 6, Appl1
24	579.5	45.9	832	3	US-08-768-859A-20	Sequence 20, Appl1
25	579.5	45.9	832	3	US-08-767-820A-20	Sequence 20, Appl1
26	579.5	45.9	832	3	US-08-622-046B-4	Sequence 4, Appl1
27	579.5	45.8	732	1	US-08-361-395-2	Sequence 2, Appl1
28	579.5	45.8	897	2	US-08-956-267A-1	Sequence 1, Appl1
29	578.5	45.8	766	5	PCT-US95-06157-9	Sequence 9, Appl1
30	578.5	45.8	832	5	PCT-US95-06157-5	Sequence 5, Appl1
31	577.5	45.7	711	3	US-08-622-046B-13	Sequence 13, Appl1
32	577.5	45.7	711	4	US-09-100-264-2	Sequence 2, Appl1
33	577.5	45.7	760	3	US-08-768-859A-7	Sequence 7, Appl1
34	577.5	45.7	760	3	US-08-767-820A-7	Sequence 7, Appl1
35	575	45.5	1504	4	US-09-280-116-1	Sequence 1, Appl1
36	574.5	45.5	711	3	US-08-622-046B-2	Sequence 2, Appl1
37	573.5	45.4	760	5	PCT-US95-06157-7	Sequence 7, Appl1
38	566	44.8	825	3	US-09-120-82-1	Sequence 1, Appl1
39	556.5	44.1	992	1	US-08-358-782D-13	Sequence 13, Appl1
40	556.5	44.1	992	2	US-08-764-527A-13	Sequence 13, Appl1
41	556.5	44.1	1462	1	US-08-358-782D-14	Sequence 14, Appl1
42	556.5	44.1	1462	2	US-08-764-527A-14	Sequence 14, Appl1
43	551.5	43.7	711	4	US-09-100-264-4	Sequence 4, Appl1
44	549.5	43.5	1729	2	US-08-844-024-1	Sequence 1, Appl1
45	549.5	43.5	1729	2	US-08-718-547-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-944-483-8
; Sequence 8, Application US/08944483
; Patent No. 6232456
GENERAL INFORMATION: 2061
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLETTIS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLISS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944, 483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1192 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-944-483-8

Alignment Scores:
Pred. No.: 3.08e-124 Length: 1192
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x US-08-944-483-8 (1-1192)

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QY 21 GluIyThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTyrLeuThrAla 40
DB 227 GAGAAAGACGGGGCTACTCTGTGGGCGACGCTCATCCGCCAGATGGCTCTGACAGCA 286
QY 41 ALAHIScysLeuLysProArgTyrIleValHISleuGlyGlnHISAsnLeuGlnIlysglu 60
DB 287 GCCCAGCTGCTCAAGCCCTCTACATAGTTCACCTGGGCGACGACCAACCTCCAGAGAG 346
QY 61 GluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHISProGlyPheAsnAsn 80
DB 347 GAGGGGCTGAGAGACCCGAGACGACCTAGCTCTCCGCCACCCCGGCTTCAACAC 406
QY 81 SerLeuProAsnLysAspHISArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
DB 407 AGCCTCCCAACAAGACCCGCAATGACATCATGCTGTGAAGATGGCATCGCCAGTC 466
QY 101 SerIleThrIleAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
DB 467 TCCATCACCTGGGCTGTGGACCCCTCACCTCTCTCACGCTGTGTCTGCTGCGAC 526
QY 121 SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHISThr 140
DB 527 AGCGGCTCATTTCCGGCTGGGAGAGACGTCACAGCCCGGCTTACGCGCTTCACAC 586
QY 141 LeuArgCysAlaAsnIleThrIleGlnHISGlnLysCysGluAsnAlaTyrProGly 160
DB 587 TTGCGATGGCCCAACATCATCATGACACAGAAAGTGTGAAGACCGCTACCCCGG 646
QY 161 AsnIleThrAspHISMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
DB 647 AACATCACACACACATGGGTGTGCCAGGCTCAGAGAGAGGGGCAAGGATCTCTCCAG 706
QY 181 GlysAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTPGly 200
DB 707 GGTGATCTCCGGGGGCTCTGTGTCTTAACCACTCTTCAAGGCTATATCTCTGGGG 766
QY 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
DB 767 CAGGATCCGGTGTGATCAACCCGAAAGCCTGTGTCTACAGAAAGTGTGCAAAATATGTG 826
QY 221 AspTyrIleGlnGlnThrArgThrMetLysAsnAsn 230
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DB 827 GACTGATCCAGAGACGATGAAGACAAAT 856

RESULT 2
US-09-025-059-2
Sequence 2, Application us/09025059
Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guebler, Neil J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTTT10
CLONE: 2723646
US-09-025-059-2

Alignment Scores:
Pred. No.: 3.57e-124 Length: 1314
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x US-09-025-059-2 (1-1314)

QY 1 ArgIleIlelysglypnehlucylsProHISerGlnProTyrGlnAlaIleuPhe 20
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DB 344 GAGAAAGACGGGCTACTCTGTGGGCGACGCTCATCCGCCAGATGGCTCTGACAGCA 403
QY 41 ALAHIScysLeuLysProArgTyrIleValHISleuGlyGlnHISAsnLeuGlnIlysglu 60
DB 404 GCCCAGCTGCTCAAGCCCTCTACATAGTTCACCTGGGCGACACCACTCCAGAGAG 463
QY 61 GluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHISProGlyPheAsnAsn 80
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Db 464 GAGGGCTGTGACACACCCGGACACCACTAGTCTTCCGCCACCCGGCTTCAACAC 523
Qy 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
Db 524 AGCTCCCAACAAAGACACCGCATGATCATGCTGGTGGMAATGGATCGCCAGTC 583
Qy 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
Db 584 TCCATCAGCTGGGCTGTGCGACCCCTCCTCCTCAGCTGTGTCAGTGTGCGGAC 643
Qy 121 SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
Db 644 AGCTGCCATCTTCGGCTGGGGACACGTCACGCCGCCAGTTACGCTTCCCTCACACC 703
Qy 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGly 160
Db 704 TTGCGATCGCCGACATACATCATCATTTAGACACGAAAGTGTGMAAGCTTACCCGGC 763
Qy 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
Db 764 AACATCAGACAGACCATGCTGTGTGCCAGCTGCAGAAAGGGGCAAGACTCTCCGACAG 823
Qy 181 GlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
Db 824 GGTGACTCGGGGGCCCTGTGCTGTACCAAGTCTTCAAGGCATTATCTCTGGGGC 883
Qy 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
Db 884 CAGATCGCTGTGCGATACACCCGAAAGCTGTGTCTTACAGAAAGTCTGCAAAATATGTG 943
Qy 221 AspTrpIleGlnIleThrMetLysAsnAsn 230
Db 944 GACTGATCCAGAGACGATGAAGAACAAT 973

RESULT 3
US-08-944-483-7
Sequence 7, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLETTIS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183 US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-944-483-7

Alignment Scores:
Pred. No.: 5,53e-123 Length: 1166
Score: 1251.00 Matches: 228
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 2
Query Match: 99.05% Indels: 0
DB: Gaps: 0

US-09-856-320a-2_copy_53_282 (1-230) x US-08-944-483-7 (1-1166)

Qy 1 ArgIleIleLysGlyPheGlnCysLysProHisSerGlnProTrpGlnAlaAlaLeuPhe 20
Db 163 AGGATCATCAAGGGGTTGAGTGCAGTGCNAGCCTCATCCAGCCCTGGAGGACAGCCCTGTTG 222
Qy 21 GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 40
Db 223 RAGAAACGGCGGTACTCTGTGGGGCGACGCTATCGCCCCCAATGATGCTCTGCACAGCA 282
Qy 41 AlaHisCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlu 60
Db 283 GCCCATCTCCCTCAAGCCCGCTACATGTTACCTGGGGCGACCAACCTTCAAGAGAG 342
Qy 61 GluLysCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 80
Db 343 GAGGCGTGTGAGACACCCGGACAGCCAGCTGATCTTCCGCCACCCCGGCTTCAACAC 402
Qy 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
Db 403 AGCTCCCAACAAAGACACCGCAATGATCATCTGTGGTGAAGATGGATCGCCAGTC 462
Qy 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
Db 463 TCCATCAGCTGGGCTGTGCGACCCCTCACCCTTCTCACCCTGTGTACCTGTGGCAC 522
Qy 121 SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
Db 523 AGCTGCTCATTTCCGGCTGGGGCAGACGTCAGCCCGCAGTTAACGCTTCCCTCACACC 582
Qy 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGly 160
Db 583 TTGCGATCGCCGACATCATCATTTAGACACGAAAGTGTGAAAGCGCTTACCCGGC 642
Qy 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
Db 643 AACATCAGACAGACCATGCTGTGTGCCAGCTGCAGAAAGGGGCAAGACTCTCCGACAG 702
Qy 181 GlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
Db 703 GGTGACTCGGGGGCCCTGTGCTGTGAACCAAGTCTTCAAGGCATTATCTCTGGGGC 762
Qy 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
Db 763 CAGGATCGGTGTGCGATACCCCGAAAGCTGTGTCTTACAGAAAGTCTGCAAAATATGTG 822
Qy 221 AspTrpIleGlnIleThrMetLysAsnAsn 230
Db 823 GACTGATCCAGAGACGATGAAGAACAAT 852

RESULT 4

US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Q1, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1052
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-10

Alignment Scores:

Pred. No.:	6, 22e-120	Length:	1052
Score:	1221.50	Matches:	223
Percent Similarity:	98.27%	Conservative:	4
Best Local Similarity:	96.54%	Mismatches:	3
Query Match:	96.71%	Indels:	1
DB:	4	Gaps:	1

US-09-856-320a-2_COPY_53_282 (1-230) x US-09-386-642-10 (1-1052)

QY 1 ArgIleIleLysGlyPheGluCys---LysProHisSerGlnProTrpGlnAlaLeu 19
DB 163 AAGATCGTGGGGGCTACAGCTGCTAGAAAGACATCCAGCCCTGGGAGGAGCCCTG 222
QY 20 PheGluLysThrArgLeuLeuGlyAlaThrLeuAlaProArgTrpLeuThr 39
DB 223 TTCGAGAGAGCGGGCTACCTGTGGGCGAGCTCTCCGCCAGATGGCTCTGACA 282
QY 40 AlaAlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLys 59
DB 283 GCAGCCGAGCTGCTCAAGCCCGCTACATGTTCTACCTGGGGAGGACCACTCCAGAG 342
QY 60 GluGluGlyCysGluGlnThrArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLys 79
DB 343 GAGGAGGCGTGTAGAGCAGCCGAGCAGCAGCTGCTCCGCCAGCTCCGCTCAAC 402
QY 80 AsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerPro 99
DB 403 AACAGCCTCCCAACAAGACCAACCGCAATGACATCATCTGTTGAAGATGSCATGCCCA 462
QY 100 ValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGly 119
DB 463 GTCATCATACCGGGGTGTGGACCCCTCACCCTCCCTCAAGCTGTGCTGCTGCTG 522
QY 120 ThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHis 139
DB 523 ACCAGCTGCTCATTTCCGGCTGGGCGAGCAGCTCCAGCCCGCAGTTACCTGCTCCAC 582
QY 140 ThrLeuArgCysAlaAsnIleThrIleGlnHisGlnLysCysGlnAsnAlaTrpPro 159
DB 583 ACCCTTGCGATGCGCCCAACATCACCATCATTTGACACAGAAAGTGTAGAAACGGCTACCC 642
QY 160 GlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCys 179
DB 643 GCGAATCATCAGACACCATGCTGTGTGCGACGCTGCGAGGAGGGGCAAGGACTCTG 702
QY 180 GlnGlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp 199
DB 703 CAGGCTGACACCGGGGCGCTGTGCTGTAAACAGACTCTTCACAGCATTTATCTCTGG 762
QY 200 GlyGlnAspProCysAlaIleThrArgLysProGlyValIleTrpLysValCysLysTrp 219

DB 763 GGCAGAGATCGTGTGAGTACACCCGAAACCTGGTGTACAGAAAGTCTCAATAT 822
QY 220 ValAspTrpIleGlnGlyThrMetLysAsnAsn 230
DB 823 GTGACTGATCCAGGAGCATGAGAACAT 855

RESULT 5

US-08-790-137-2
; Sequence 2, Application US/08790137
; Patent No. 5840871

GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
; TITLE OF INVENTION: KALLIKREIN
; NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/790,137
FILING DATE: Filed Herewith
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0195 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-790-137-2

Alignment Scores:

Pred. No.:	1, 03e-119	Length:	833
Score:	1218.00 <td>Matches:</td> <td>220</td>	Matches:	220
Percent Similarity:	97.83%	Conservative:	5
Best Local Similarity:	95.65%	Mismatches:	0
Query Match:	96.44%	Indels:	0
DB:	2	Gaps:	0

US-09-856-320a-2_COPY_53_282 (1-230) x US-08-790-137-2 (1-833)

QY 1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPhe 20
DB 96 CGATGTGTGGAGGCTGTGAGTGTGAGCAGCATTTCCAGCCCTGGCAGCGGCTGTAC 155
QY 21 GluLysThrArgLeuLeuGlyAlaThrLeuAlaProArgTrpLeuThrAla 40
DB 156 CAGAAACCGGCTACTCTGTGGGCGAGGNTCATNGCCCCAGATGTTCTTCAAGCA 215
QY 41 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
DB 216 GCCACCTGCTTNAAGCCCGCTACATAGTTACCTGGGCGAGCAGACCACTCCAGAGAG 275

QY 61 GluLysGluGlnThrAlaThrGluSerPheProHisProGlyPheAsnAsn 80
Db 276 GAGGGCTGTGAGCAGACCCGACAGCCAGTGTCTTCCCGCCAGCCGCTTCAACAC 335
QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
Db 336 AGCCTCCCAACAAAGACCCGCAATGATCATGCTGGTGAAGATGGATGCGCCAGTC 395
QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
Db 396 TCCATCAACCTGGCTGTGCGACCCCTCACCCCTCTCCACGCTGTGACATGCTGGACG 455
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
Db 456 AGCTGCTCATTTCCGGCTGGGCGACAGCCAGCCCGAGTACCCCTGCTCACACC 515
QY 141 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGly 160
Db 516 TTGGGATGCGCCACATCATCATATGAGCAGCAAGATGTGAGAAAGGCTTACCCGCG 575
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGln 180
Db 576 AACATCACAGACACCATGCTGTGCGACGCTGAGGAAGGGGCGCAAGACTCTGCGCAG 635
QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
Db 636 GGTGACCTCCGGGGGCGCTGTGCTGTACACAGCTCTTCAAGGCAATTAATCTCTGGG 695
QY 201 GluAspProCysAlaIleThrArgLysProGlyValLysTrpThrLysValCysLysTrpVal 220
Db 696 CAGATCATCGTGTGAGTACACCCGAAAGCTGTGTCTTACAGAAAGTCTGCAATATGTG 755
QY 221 AspTrpIleGlnLysThrMetLysAsnAsn 230
Db 756 GACTGATCCAGAGACGATGAAGAACAAT 785

P.D. Dec 18, 2001

A-102e

RESULT 6
US-09-280-116-3
; Sequence 3, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-3

Alignment Scores:
Pred. No.: 4, 8e-88 Length: 618
Score: 916.50 Matches: 184
Percent Similarity: 90.788 Conservative: 3
Best Local Similarity: 89.328 Mismatches: 4
Query Match: 72.578 Indels: 16
Gaps: 2

US-09-856-320a-2_copy_53_282 (1-230) x US-09-280-116-3 (1-618)

QY 24 ArgLeuLeuGlyGlyAlaThrLeuIleAlaPro-ArgTrpLeuLeuThrAlaAlaHisCys 43
Db 2 CGGCTACTCTGTGGGGGACCC---TCATCCCTTCAGATGCTCTGACACACACCCACTG 58
QY 43 sLeuLysProArgTrpTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCys 63
Db 59 CCTCAAGCCCGGCTACTACTGCTACCTGGGCGACACACCTCAAGAAAGAGAGGCGCTG 118

QY 63 sGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuPr 83
Db 119 TGACGACACCCGAGACAGCAGCTGATCTTCCCGCCAGCCGCTTCAACACACCTCC 178
QY 83 AsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal-SerIleTr 103
Db 179 CACAAAGACCCAGCATGATCATGCTGTGAAAGATGGCATGCGCAGTGCATCA 238
QY 103 hTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysL 123
Db 239 CTGGGCTGTGCGACCCCTTACCCCTCTCTATGCTGTGTACTGTGACACAGTGC 298
QY 123 euIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArgC 143
Db 299 TCATTTCCGGCTGGGCGACAGCCGTCAGCCCGCAGTTACGCTCTCCACACCTGGGAT 358
QY 143 yAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsnIleTr 163
Db 359 GCGCAACATCATCATATGAGCAGCAAGATGTGAGAAAGGCTTACCCGCGCAACATCA 418
QY 163 hAspThrMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGlnLysAsps 183
Db 419 CAGACACCATGCTGTGTGCGACGCTGAAGAAAGGGGCGCAAGACTCTGCGCAA----- 471
QY 183 ergLysGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp-GlyGlnAsp 202
Db 472 -----GTCCTTC-AAAGCATTAATCTCTGGGCGCGACAGAC 507
QY 203 -ProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpValAspTr 222
Db 508 TCCGTGTGATCATCACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAAAATATGTGACTG 567
QY 222 pIleGlnGlu 225
Db 568 GATCCAGGAA 577

P.D. 2006

RESULT 7
US-09-070-526-1
; Sequence 1, Application US/09070526
; Patent No. 6100059
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CLINKENBEARD, HELEN
; TITLE OF INVENTION: BURGESS, NICOLA
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,526
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711952.3
; FILING DATE: 9-JUN-1997
; APPLICATION NUMBER: EP 97309646.4
; FILING DATE: 1-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30353
; TELECOMMUNICATION INFORMATION:

A-102e

Db 712 CTC-----CACCTGGCCACTTAACGACCTCATGCTCATCAAACTGAAACAG 759
Qy 98 rProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAl 118
Db 760 AAGATTGTCCTCCACTAAAGATGTCAGACCATCAAGCTCTCTCTATTGTCCCTGCG 819
Qy 118 aGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuPr 138
Db 820 TGGGACAAAGTGTGTGGTGTCCGGCTGGGGACAAACCAAGAGCCCAAGTGCACCTGCC 879
Qy 138 ohIstHleuArgCysAlaAsnIleThrIleIleGlnHisIleGlnCysGluAsnAlaTy 158
Db 880 TAAAGTCTCCAGTGTCTGAATATCAGGCTCTAAGTCAGAAAGTGTGAGATGCTTA 939
Qy 158 rProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyAspSe 178
Db 940 CCCGAGACAGATAGATGACACATGTTCTGCGCGGT---GACAAAGAGGTAGAGACTC 996
Qy 178 rCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSe 198
Db 997 CTGCAGAGGTATCTGGGGGCGCTGTGCTGCAATGGCTCCCTGCAGGAGTCTGTCTC 1056
Qy 198 rTrpGlyGlnAspProCysAlaIleThrArgLeuProGlyValThrTrpValCysGly 218
Db 1057 CTGGGAGATTATACCTGTGTGCGCGCCCAACAGACCGGGGTCTACGAACTCTGCAA 1116
Qy 218 sTyValAspTrpIleGlnGlnIleThrMetLeuAsnAsn 230
Db 1117 GTTCACCAAGTGTATCCAGGAACCATTCACAGGCCAAC 1153
RESULT 12
US-09-280-116-20/c
: Sequence 20, Application US/09280116A
: Patent No. 6331427
: GENERAL INFORMATION:
: APPLICANT: Robison, Keith E.
: TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
: FILE REFERENCE: 5800-24, 035800/176965
: CURRENT APPLICATION NUMBER: US/09/280,116A
: CURRENT FILING DATE: 1999-03-26
: NUMBER OF SEQ ID NOS: 268
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 1364
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: trypsin-like serine proteases
: NAME/KEY: misc-feature
: LOCATION: (1)..(1364)
: OTHER INFORMATION: n = a, t, c, or g
US-09-280-116-20
Alignment Scores:
Pred. No.: 1,01e-57 Length: 1364
Score: 634.50 Matches: 123
Percent Similarity: 64.82% Conservative: 41
Best Local Similarity: 48.62% Mismatches: 60
Query Match: 50.24% Indels: 29
Gaps: 3
US-09-856-320A-2_COPY_53_282 (1-230) x US-09-280-116-20 (1-1364)
Qy 5 GlyHeuGlyCysLysProHisSerGlnProTrpGlnAlaLeuPheGlnLysThrArg 24
Db 828 GGGTACACCTGCTCCCTCCACTTCACGCCCTGGCAGCGTCCCTACATGACAGGGGGG 769
Qy 25 LeuLeuGlyGlyAlaThr-LeuIleAlaProArgTrpLeuThrAlaAlaHisCysLe 44
Db 768 CTACTCTGTGGGAGAGCTGCTGTCACCCCAATGGTCTCTACTGCGGACACTGTCT 709
Qy 44 uLysProArgTrpTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysG 64

Db 708 AAAGAGGGGCTCAAAAGTTTACTAGCCAGCACGCCCTAGGCGGTGTGGAAGCTGTGGA 649
Qy 64 uGlnThrArgThrAlaThrGlnUserPheProHisProGlyPheAsnAsnSerLeuProAs 84
Db 648 GCAGGTGAGGAGAGTGTCCACTCTATCCGCCACCTTAATAGAGAGAGAGAGAGAGAGAG 589
Qy 84 nLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTr 104
Db 588 CCTGACACCAACCATGATCATCTCTCTGTGAGTGTGAGTCCCGGTCCAGCTCAGCAGG 529
Qy 104 pAlaValArgProLeuThrLeuSer---SerArgCysValThrAlaGlyThrSerCysLe 123
Db 528 CTACATCCAAACCTGCGCCCTTCCACACAAACCGGCTTAACCCCTGGACACACCTGTGC 469
Qy 123 uIleSerGlyTrpGlySerThrSerSerProGln-----LeuArg 136
Db 468 GGTCTGTGGTGGGACACACCACCCAGGAGGTATGACACCCACAGGTGCTGAG 409
Qy 136 g-----Le 137
Db 408 GCCCATAGAGTGTGGGGAACAGGGGACAGATGGAGGAGAGGTCTGATGATTT 349
Qy 137 uProHis-ThrLeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsn 157
Db 348 ACCCAAAACCTCTACAAATGTGCCAAATCAACTTCGCTGATGATGAGAGTGTGCTCAAG 289
Qy 157 lAtyTrpGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLys 177
Db 288 TCTACCCAGGAAGATCTCACTGACCAATGTTGTGTGGCGGACAAACAAAGGTGGCAAG 229
Qy 177 sPserCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 197
Db 228 ACTCTGTGAGAGGTGACTCTGGGGGCCCTGTGTGTGAAGAACAATGTATGACATCG 169
Qy 197 lSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrTrpValC 217
Db 168 TCTCTGTGGGAGACTTCCCATGTGGGCAACTGACCGGCGTGTGTACACCCGTGTCT 109
Qy 217 yLysTrpValAspTrpIleGlnGlnIleThrMetLys 228
Db 108 CAAGTATGCTCTGTGATCCGTGAACAAATCCGA 74
RESULT 13
US-08-768-859A-9
: Sequence 9, Application US/08768859A
: Patent No. 6013471
: GENERAL INFORMATION:
: APPLICANT: Tindall, Donald J.
: APPLICANT: Young, Charles Y.F.
: APPLICANT: Saedi, Mohammed S.
: TITLE OF INVENTION: DNA Encoding HK2 Variant Polypeptides
: NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,859A
FILING DATE: 17-DECEMBER-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 545,002US3


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Db 259 AGCCTTCGAAGACATCAAGCCTTAGACAGATGACAGATCCAGGCAATGACCTCAGCTG 318
Qy 94 VallyMetalaserProvalserIleThrPrAlaValArgProLeuThrLeuSerSer 113
Db 319 CTCGCCCTGTGACAGCTGCCAAGATCAAGATGTTGGAAGAGCTCTGGCCCTGCCACAC 378
Qy 114 ArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrPglySerThrSerPro 133
Db 379 CAGGAGCCAGCACTGGGAGCCACCTGCTACAGCCTGAGCCTGGGCGAGATCGAACAGAG 438
Qy 134 GlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleGlnHisGlnLys 153
Db 439 GAGTTCCTTCCGCCAGGAGCTTCAGTGTGAGCTGCATCTCTCCATACATGACATG 498
Qy 154 CysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnLys 173
Db 499 TGTGCTAGAGCTTACTCTGAGAAGGTGACAGATCATGTTGTGTGCGGTCTGGAC 558
Qy 174 GlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeu 193
Db 559 GGTGTTAAAGACACTTGTGGGGGTGATCTGGGGGTCCACATGCTGTAATGTGTGCT 618
Qy 194 GlnGlyIleIleSerThrGlyGlnAspProCysAlaIleThrArgLysProGlyValTyr 213
Db 619 CAAGGTATCATCATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 678
Qy 214 ThrLysValCysLysTyrValAspThrIleGlnIleThrMetLysAsn 230
Db 679 ACCAAGGTGTGATTTACCGGAAGTGAATCAAGACACCATGCGAGCCAC 729

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RESULT 15
US-08-622-046B-17
Sequence 17, Application US/08622046B
Patent No. 6103237
GENERAL INFORMATION:
APPLICANT: Saedi, Mohammed S.
APPLICANT: Mikolajczyk, Stephen D.
TITLE OF INVENTION: Stable Variant HK2 Polypeptide
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Moessner & Klueh, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622.046B
FILING DATE: 26-MARCH-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Moessner, Warren D.
REGISTRATION NUMBER: 30.440
REFERENCE/DOCKET NUMBER: 476.001US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6903
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 766 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..732
US-08-622-046B-17

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Alignment Scores:
Pred. No.: 1.32e-52 Length: 766
Score: 582.50 Matches: 107
Percent Similarity: 62.87% Conservative: 42
Best Local Similarity: 45.15% Mismatches: 81
Query Match: 46.12% Indels: 7
DB: 3 Gaps: 1

US-09-856-320A-2_COPY_53_282 (1-230) x US-08-622-046B-17 (1-766)
Qy 1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTyrGlnAlaLeuPhe 20
Db 19 CGGATTTGGGAGGAGCTGGGAGGTGTGAGAAGCATTTCCCAACCTGGCAGGTGTGTAC 78
Qy 21 GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuLeuThrAla 40
Db 79 AGTCATGATGGGCACTGTGGGGGTGCTCCGTGCAACCCCAAGTGGGTGCTCACAGCT 138
Qy 41 AlaHisCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlu 60
Db 139 GCCCATTCCTTAAGAAAGATAGCCAGGTGTGCTGGGTGGGCGGACACACTGTTAGCCT 198
Qy 61 GluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 80
Db 199 GAAAGACAGGCGCAGAGGAGGTCCTGTCAGCCACACTTCCACACCCGCTTACAAATAG 258
Qy 81 SerLeu-----ProAsnLysAspHisArgAsnAspIleLeuLeu 93
Db 259 AGCCTTCGAAGACATCAAGCCTTAGACCAATGAAGACTCCAGCAGCATCTCATATGCTG 318
Qy 94 VallyMetalaserProvalserIleThrPrAlaValArgProLeuThrLeuSerSer 113
Db 319 CTCGCCCTGTGACAGCTGCCAAGATCAAGATGTTGGAAGAGCTCTGGCCCTGCCACAC 378
Qy 114 ArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrPglySerThrSerPro 133
Db 379 CAGGAGCCAGCACTGGGAGCCACCTGCTACAGCCTGAGCCTGGGCGAGATCGAACAGAG 438
Qy 134 GlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleGlnHisGlnLys 153
Db 439 GAGTTCCTTCCGCCAGGAGCTTCAGTGTGAGCTGCATCTCTCCATACATGACATG 498
Qy 154 CysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnLys 173
Db 499 TGTGCTAGAGCTTACTCTGAGAAGGTGACAGATCATGTTGTGTGCGGTCTGGAC 558
Qy 174 GlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeu 193
Db 559 GGTGTTAAAGACACTTGTGGGGGTGATCTGGGGGTCCACATGCTGTAATGTGTGCT 618
Qy 194 GlnGlyIleIleSerThrGlyGlnAspProCysAlaIleThrArgLysProGlyValTyr 213
Db 619 CAAGGTATCATCATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 678
Qy 214 ThrLysValCysLysTyrValAspThrIleGlnIleThrMetLysAsn 230
Db 679 ACCAAGGTGTGATTTACCGGAAGTGAATCAAGACACCATGCGAGCCAC 729

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Search completed: December 23, 2002, 16:03:53
Job time : 73 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 13:07:57 ; Search time 80 Seconds

(without alignments)
383.096 Million cell updates/sec

Title: us-09-856-320a-2_COPY_53_282

Perfect score: 1263
Sequence: 1 RLKGFCKPHSQPQWQALF.....GVYTKVCKYVDWIQETMKNN 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1263	100.0	250	21	Human TLSP. Homo
2	1263	100.0	250	21	Human PRO1279 (UNQ)
3	1263	100.0	250	22	Human secreted pro
4	1263	100.0	250	22	Human PRO1279 poly
5	1263	100.0	250	22	Protein of the Inv
6	1263	100.0	250	23	Prostate cancer-as
7	1263	100.0	250	23	Human angiotensin
8	1263	100.0	250	23	Human PRO1279 prot
9	1263	100.0	250	23	Human PRO protein,
10	1263	100.0	282	20	CASB12 amino acid

11	1263	100.0	282	21	AA111712	Human serine prote
12	1263	100.0	282	21	AA43636	A human prostate-a
13	1257	99.5	281	20	AA42440	CASB12 polypeptide
14	1240.5	98.2	275	21	AA111714	Human serine prote
15	1236	97.9	228	21	AA111712	Human TLSP. Homo
16	1233	97.6	250	20	AA36093	Extended human sec
17	1232	97.5	248	22	AA108017	Human PS13 consen
18	1221.5	96.7	289	22	AA16483	Fusion gene with h
19	1221.5	96.7	289	22	AA16483	Amino acid sequenc
20	1067	84.5	276	21	AA111713	Mouse serine prote
21	739	58.5	250	21	AA121298	Human KLK-L3 prote
22	739	58.5	251	22	AA116971	Human novel secret
23	737	58.4	247	22	AA123217	Human novel enzyme
24	734.5	58.2	256	21	AA121297	Human KLK-L3 prote
25	719	56.9	247	22	AA108677	Human human connec
26	719	56.9	247	22	AA123752	Human novel enzyme
27	719	56.9	247	22	AA117043	Human novel secret
28	690	54.6	275	21	AA121311	Human neuropsin.
29	686	54.3	260	17	AA110694	Human recombinant
30	686	54.3	260	18	AA112393	Mouse neuropsin pr
31	686	54.3	260	18	AA112393	Mouse ischemic co
32	684	54.2	256	23	AA179390	Novel human kallik
33	684	54.2	320	23	AA182732	Human protease, PR
34	684	54.2	320	23	AA182732	Amino acid sequenc
35	683	54.1	260	20	AA141744	Human PRO1272 prote
36	683	54.1	260	20	AA132852	Human serine prote
37	683	54.1	260	20	AA132852	Human acid sequenc
38	683	54.1	260	20	AA187703	A human serine pro
39	683	54.1	260	21	AA121322	Human neuropsin.
40	683	54.1	260	21	AA144300	Human PRO1322 (UNQ)
41	683	54.1	260	21	AA151131	Human neuropsin pr
42	683	54.1	260	22	AA151131	Human human diagno
43	683	54.1	260	22	AA151131	Human PRO1322 poly
44	683	54.1	260	22	AA151087	Human angiotensin
45	683	54.1	260	23	AA195458	Human angiotensin

ALIGNMENTS

RESULT 1	AA121325	
ID	AA121325 standard; Protein; 250 AA.	
XX	AA121325:	
XX	02-FEB-2001 (first entry)	
XX	Human TLSP.	
XX	Human: KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; TLSP;	
KW	trypsin-like serine protease; kallikrein-like protein; serine protease;	
KW	cytostatic; cancer; prostate cancer.	
XX	Homo sapiens.	
OS	MO200053776-A2.	
XX	14-SEP-2000.	
XX	09-MAR-2000; 2000MO-CA00258.	
XX	11-MAR-1999; 99US-0124260.	
PR	01-APR-1999; 99US-0127386.	
PR	21-JUL-1999; 99US-0144919.	
XX	(MOUN) MOUNT SINAI HOSPITAL.	
PI	Yousef GW, Diamandis EP;	
XX	WPI; 2000-567440/55.	
XX	New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L	

PT protein mediated disorders, especially cancer. -
XX
PS Example 5; Fig 27; 184pp; English.
XX
CC The present sequence is human trypsin-like serine protease (TLSP), a
CC member of the serine protease family. Kallikreins and
CC kallikrein-like proteins are a subgroup of the serine protease enzyme
CC family. They catalyse the selective cleavage of specific polypeptide
CC precursors to release peptides with potent biological activity. Nucleic
CC acids encoding kallikrein-like proteins KLK-11, KLK-12, KLK-13, KLK-14,
CC KLK-15 and KLK-16 have been isolated. The proteins are useful in the
CC treatment, monitoring and diagnosis of cancers, especially prostate
CC cancer. They can also be used to identify a substance that can associate
CC with or mediate the biological activity of the proteins. Antibodies can
CC be used to treat conditions mediated by the kallikrein-like proteins.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 1263; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIIFGFECKRHSOPWQALFEKTRLLCGATLIAPRWLLTFAHCLKPRYIYHLGOHNLQKE 60
DB 21 RIIFGFECKRHSOPWQALFEKTRLLCGATLIAPRWLLTFAHCLKPRYIYHLGOHNLQKE 80
QY 61 EGCEQRTFATESFPHPGFNNSLPKNDHRNDIMLVKASPVSIWAVRPLTSSRCVTAGT 120
DB 81 EGCEQRTFATESFPHPGFNNSLPKNDHRNDIMLVKASPVSIWAVRPLTSSRCVTAGT 140
QY 121 SCLISGSGTSSPOLRLPHRLRCANITIIHOCENAYPGNIDTMCASVOEGSKDSCQ 180
DB 141 SCLISGSGTSSPOLRLPHRLRCANITIIHOCENAYPGNIDTMCASVOEGSKDSCQ 200
QY 181 GDSGGPLVQNSLOGISMGODPCAITRKPGYTKVCKYDWMIOETKNN 230
DB 201 GDSGGPLVQNSLOGISMGODPCAITRKPGYTKVCKYDWMIOETKNN 250
RESULT 2
ID AAY93390
XX AAY93390 standard; Protein; 250 AA.
AC AAY93390;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1279 (UNC649) amino acid sequence SHQ ID NO:170.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW Transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.
PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.

PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
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PR 15-SEP-1998; 98US-0100388.
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PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
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PR 17-SEP-1998; 98US-0100683.
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PR 17-SEP-1998; 98US-0100930.
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PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
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PR 23-SEP-1998; 98US-0101477.
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PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102584.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.

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PR	27-OCT-1998;	98US-0106062.
PR	28-OCT-1998;	98US-0106023.
PR	28-OCT-1998;	98US-0106029.
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PR	28-OCT-1998;	98US-0106178.
PR	29-OCT-1998;	98US-0106248.
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PR	30-OCT-1998;	98US-0106464.
PR	03-NOV-1998;	98US-0106856.
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PR	18-NOV-1998;	98US-0108858.
PR	18-NOV-1998;	98US-0108904.

PI	Baker K	Goddard A,	Gurney AL,	Smith V,	Watanabe CK,	Wood WI;
XX	WPI:	2000-237871/20.				
DR	N-PSDB:	AAA37072.				
XX	New mammalian DNA sequences encoding transmembrane, receptor or					
PT	secreted PRO polypeptides, useful for screening of potential peptide or					
PT	small molecule inhibitors of the relevant receptor/ligand interactions					
XX	ClaIm 12; Fig 102; 773pp; English.					
PS	AAA37022 to AAA37144 encode the new isolated human transmembrane,					
XX	receptor or secreted PRO polypeptides given in AA999340 to AA99462. The					
CC	transmembrane and receptor PRO proteins can be used for screening of					
CC	potential peptide or small molecule inhibitors of the relevant					
CC	receptor/ligand interactions. The polypeptides and nucleotide sequences					
CC	encoding them have various industrial applications, including uses as					
CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent					
CC	PCR primers and hybridisation probes used in the isolation of the PRO					
CC	polypeptides from the present invention.					
XX	Sequence	250 AA;				
SQ	Query Match	100.0%;	Score 1263;	DB 21;	Length 250;	
	Best Local Similarity	100.0%;	Pred. No. 2e-113;			
	Matches 230;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 RIIRGFECKPHSPQMOALFEKTRLLGCATLIAPRMLITAAHCLPKRYIVHIGQHNLOKE 60					
Db	21 RIIRGFECKPHSPQMOALFEKTRLLGCATLIAPRMLITAAHCLPKRYIVHIGQHNLOKE 80					
OY	61 EGCQOTRATISFFHPGNGNNSLPNKDHNDIMLYKMASPVSTIAWVRPLTSSRCVYTAGT 120					
	81 EGCQOTRATISFFHPGNGNNSLPNKDHNDIMLYKMASPVSTIAWVRPLTSSRCVYTAGT 140					

Oy	121	SCLSISGMCSTSSPOLRLPHILTRCANTITIEHOCENNAPEPNTIDTWCASSVOEGGDSQ	180
Db	141	SCLSISGMCSTSSPOLRLPHILTRCANTITIEHOCENNAPEPNTIDTWCASSVOEGGDSQ	200
Oy	181	GDSGGPLVCNCSLGGIISWGDPCATIRKPGVYTKYCKYVDWIQETMKNN	230
Db	201	GDSGGPLVCNCSLGGIISWGDPCATIRKPGVYTKYCKYVDWIQETMKNN	250
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ID	ABB50479	standard; Protein: 250 AA.	
XX	NC	ABB50479;	
DT	07-FEB-2002	(first entry)	
DE	Human secreted protein encoded by gene 179 SEQ ID NO:427.		
KW	Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;		
KW	dermatological; immunosuppressive; antileukemia; immunostimulant;		
KW	cytotoxic; cardiant; vascular; anti-angiogenic; ophthalmological;		
KW	neuroprotective; nontropic; anticonvulsant; antialzheimers; vulnery;		
KW	antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;		
KW	multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;		
KW	human immunodeficiency virus; hyperproliferative disorder; wound healing		
KW	Gaucher's disease; cardiovascular disease; Schmitz syndrome; chemotaxis		
KW	Chagas's cardiomyopathy; coronary arteriosclerosis; angiodysplasia;		
KW	corneal graft neovascularisation; diabetic retinopathy; regeneration;		
KW	neurological disorder; Huntington's chorea; Alzheimer's disease;		
XX	Parkinson's disease; infectious disease.		
OS	Homo sapiens.		
PN	WO200162891-A2.		
PD	30-AUG-2001.		
XX	21-FEB-2001; 2001WO-US05614.		
PE	24-FEB-2000; 2000US-184836P.		
PR	29-MAR-2000; 2000US-193170P.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
PA	NI J, Ebner R, Lafleur DM, Moore PA, Olsen HS, Rosen CA;		
PI	Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;		
PI	Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferris AM, Fan P;		
PI	Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;		
PI	Zeng Z, Greene JM;		
XX	WPI: 2001-625724/72.		
DR	N-PSDB: ABA83372.		
XX	Nucleic acids encoding 207 human secreted polypeptides, useful for		
PT	preventing, diagnosing and/or treating, e.g. cancers, Parkinson's		
PT	disease and diabetic retinopathy -		
XX	Claim 11: Page 1181-1182; 1533pp; English.		
XX	ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted		
CC	proteins (I) and polynucleotide (II) sequences. (I) and (II) have various		
CC	activities based on the tissues and cells the genes are expressed in.		
CC	Example of these activities include: immunomodulatory; antisclerotic;		
CC	dermatological; immunosuppressive; antiinflammatory; immunostimulant;		
CC	anti-HIV; cytotoxic; cardiant; anti-angiogenic; ophthalmological;		
CC	neuroprotective; nontropic; anticonvulsant; antialzheimers; vascular;		
CC	antiparkinsonian; antimicrobial; and vulnery. (I) and (II) can be used		
CC	in gene therapy and vaccine production. (I) and (II) can be used in the		
CC	prevention, diagnosis and treatment of immune disorders (e.g. multiple		
CC	sclerosis, systemic lupus erythematosus and human immunodeficiency virus		
CC	(HIV) infections), hyperproliferative disorders (e.g. cancers and		

CC Gaucher's disease), cardiovascular diseases (e.g. Sclimtar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiodysplastic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA8185 to
 CC ABA8193 and ABB50300 represent sequences used in the exemplification of
 CC the present invention.
 CC
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1263; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-113;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIIRGFECCKPHSQPQWQALFEKTRILCGATLIAPRWLLTAHCLKPRYIYHLOHNLQKE 60
 DB 21 RIIRGFECCKPHSQPQWQALFEKTRILCGATLIAPRWLLTAHCLKPRYIYHLOHNLQKE 80
 QY 61 EGCQRTTATESFPHPGFNNSLPNKDRNDIMLVKMA SPVSTIWA VRLTLSSRCVTAGT 120
 DB 81 EGCQRTTATESFPHPGFNNSLPNKDRNDIMLVKMA SPVSTIWA VRLTLSSRCVTAGT 140
 QY 121 SCLISGSGSTSSPOLRLPHTLRCA NITIIIEHOKCENAYPGNITDTWVCASVQEGGKDSQ 180
 DB 141 SCLISGSGSTSSPOLRLPHTLRCA NITIIIEHOKCENAYPGNITDTWVCASVQEGGKDSQ 200
 QY 181 GDSGGPLVCMQSLQGIISWGODPCATIRKPGVYTKCKYVDWIOETMKN 230
 DB 201 GDSGGPLVCMQSLQGIISWGODPCATIRKPGVYTKCKYVDWIOETMKN 250
 RESULT 4
 AAU12424
 ID AAU12424 standard; Protein: 250 AA.
 XX
 AC AAU12424;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human PRO1279 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000MO-US32678.
 XX
 PR 01-DEC-1999; 99MO-US28301.
 PR 01-DEC-1999; 99MO-US28634.
 PR 02-DEC-1999; 99MO-US28551.
 PR 02-DEC-1999; 99MO-US28564.
 PR 02-DEC-1999; 99MO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99MO-US30095.
 PR 20-DEC-1999; 99MO-US30911.
 PR 20-DEC-1999; 99MO-US30999.
 PR 30-DEC-1999; 99MO-US31243.
 PR 06-JAN-2000; 2000MO-US00377.
 PR 06-JAN-2000; 2000MO-US00376.
 PR 11-FEB-2000; 2000MO-US03565.
 PR 18-FEB-2000; 2000MO-US04341.
 PR 18-FEB-2000; 2000MO-US04342.
 PR 22-FEB-2000; 2000MO-US04414.
 PR 24-FEB-2000; 2000MO-US04914.
 PR 24-FEB-2000; 2000MO-US05004.

PR 01-MAR-2000; 2000MO-US05601.
 PR 20-MAR-2000; 2000MO-US07317.
 PR 21-MAR-2000; 2000MO-US07532.
 PR 17-MAR-2000; 2000MO-US08439.
 PR 17-MAR-2000; 2000MO-US13705.
 PR 22-MAY-2000; 2000MO-US14042.
 PR 30-MAY-2000; 2000MO-US14941.
 PR 02-JUN-2000; 2000MO-US15264.
 PR 10-NOV-2000; 2000MO-US30873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Beresini M, DeGeorge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI: 2001-408281/43.
 XX N-P-SDB; AAS21496.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 12; Fig 506; 813p; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1263; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-113;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIIRGFECCKPHSQPQWQALFEKTRILCGATLIAPRWLLTAHCLKPRYIYHLOHNLQKE 60
 DB 21 RIIRGFECCKPHSQPQWQALFEKTRILCGATLIAPRWLLTAHCLKPRYIYHLOHNLQKE 80
 QY 61 EGCQRTTATESFPHPGFNNSLPNKDRNDIMLVKMA SPVSTIWA VRLTLSSRCVTAGT 120
 DB 81 EGCQRTTATESFPHPGFNNSLPNKDRNDIMLVKMA SPVSTIWA VRLTLSSRCVTAGT 140
 QY 121 SCLISGSGSTSSPOLRLPHTLRCA NITIIIEHOKCENAYPGNITDTWVCASVQEGGKDSQ 180
 DB 141 SCLISGSGSTSSPOLRLPHTLRCA NITIIIEHOKCENAYPGNITDTWVCASVQEGGKDSQ 200
 QY 181 GDSGGPLVCMQSLQGIISWGODPCATIRKPGVYTKCKYVDWIOETMKN 230
 DB 201 GDSGGPLVCMQSLQGIISWGODPCATIRKPGVYTKCKYVDWIOETMKN 250
 RESULT 5
 AAB66139
 ID AAB66139 standard; protein: 250 AA.

```

XX AC AAB6139;
XX DT 02-APR-2001 (first entry)
XX DE Protein of the invention #51.
XX KW Secreted; transmembrane; gene therapy.
XX OS Unidentified.
XX PN WO200078961-A1.
XX PD 28-DEC-2000.
XX PF 18-FEB-2000; 2000WO-US04342.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 29-OCT-1999; 99US-0162506.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 02-DEC-1999; 99WO-US28551.
XX PR 16-DEC-1999; 99WO-US30095.
XX PR 05-JAN-2000; 2000WO-US00219.
XX PR 06-JAN-2000; 2000WO-US00376.
XX PA (GETH ) GENENTECH INC.
XX PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
XX PI Watanabe CK, Williams PM, Wood WI;
XX DR WPI: 2001-071395/08.
XX PT Secreted and transmembrane proteins and nucleic acids designated PRO,
XX PT useful as hybridization probes, in chromosome and gene mapping and gene
XX PT therapy -
XX PS Claim 1; Fig 102; 787pp; English.
XX CC The present invention relates to secreted and transmembrane proteins.
XX CC These proteins and the DNA encoding them may be used as hybridization
XX CC probes, in chromosome and gene mapping and in the generation of
XX CC anti-sense RNA and DNA. They may also be used to generate either
XX CC transgenic animals or knockout animals which are in turn useful for
XX CC development and screening of therapeutically useful reagents.
XX CC The nucleic acids may also be used in gene therapy.
XX SQ Sequence 250 AA;
SQ Query Match 100.0%; Score 1263; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIINGFECKPHSOPWQALFEKTRILCGATLIAPRWLLTAHCKLPRIYVHGLGHNLOKE 60
DB 21 RIINGFECKPHSOPWQALFEKTRILCGATLIAPRWLLTAHCKLPRIYVHGLGHNLOKE 80
QY 61 EGCBOTRTATSPFPHGFGNSLPPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTAGT 120
DB 81 EGCBOTRTATSPFPHGFGNSLPPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTAGT 140
QY 121 SCLISGMSSTSPOLRLPHTRLCANITITIEHOKCENAPGNTITPMVCAVQEGGKDSQ 180
DB 141 SCLISGMSSTSPOLRLPHTRLCANITITIEHOKCENAPGNTITPMVCAVQEGGKDSQ 200
QY 181 GDSGSPVLCNCSLOGIISWGODPCATRRKPGVYTRKVCXYVMIOETMKN 230
DB 201 GDSGSPVLCNCSLOGIISWGODPCATRRKPGVYTRKVCXYVMIOETMKN 250

```

```

RESULT 6
ID AAB61816 standard; Protein; 250 AA.
XX AC AAB61816;
XX DT 15-AUG-2002 (first entry)
XX DE Prostate cancer-associated protein #17.
XX KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
XX OS Mammalia.
XX PN WO200230268-A2.
XX PD 18-APR-2002
XX PF 12-OCT-2001; 2001WO-US32045.
XX PR 13-OCT-2000; 2000US-0687576.
XX PR 08-DEC-2000; 2000US-0733288.
XX PR 08-DEC-2000; 2000US-0733742.
XX PR 24-JAN-2001; 2001US-263957P.
XX PR 16-MAR-2001; 2001US-276791P.
XX PR 16-MAR-2001; 2001US-276888P.
XX PR 06-APR-2001; 2001US-281922P.
XX PR 24-APR-2001; 2001US-286214P.
XX PR 30-APR-2001; 2001US-08477046.
XX PR 04-MAY-2001; 2001US-288589P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX DR WPI: 2002-471335/50.
XX DR N-PSDB; ABK92131.
XX PT Detecting a prostate cancer-associated transcript in a cell in a
XX PT patient, useful for diagnosing prostate cancer (PC) or screening
XX PT modulators of PC, by determining if prostate cancer-associated genes
XX PT are expressed in a prostate tissue -
XX PS Claim 27; Page 314; 436pp; English.
XX CC The present invention relates to methods of detecting a prostate
XX CC cancer-associated transcript in a cell from a patient. The method
XX CC comprises contacting a biological sample from the patient with
XX CC prostate cancer-associated polynucleotides (designated PC genes) that
XX CC selectively hybridise to a sequence that is at least 80% identical
XX CC to them. The prostate cancer-associated polynucleotide sequences
XX CC are differentially expressed in prostate tumour tissue or in
XX CC prostate cancer and are derived from the tissues of various
XX CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
XX CC The methods of the invention are useful for diagnosing and treating
XX CC prostate cancer in mammals. The prostate cancer-associated genes are
XX CC useful for diagnosing or treating prostate cancer, as well as for
XX CC identifying modulators of prostate cancer or agents that inhibit
XX CC prostate cancer. The nucleic acid sequences are particularly useful
XX CC in gene therapy, as a vaccine or in antisense applications.
XX CC AAB61800-AAB61944 represent prostate cancer-associated proteins.
XX SQ Sequence 250 AA;
SQ Query Match 100.0%; Score 1263; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIINGFECKPHSOPWQALFEKTRILCGATLIAPRWLLTAHCKLPRIYVHGLGHNLOKE 60
DB 21 RIINGFECKPHSOPWQALFEKTRILCGATLIAPRWLLTAHCKLPRIYVHGLGHNLOKE 80

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QY 61 EGCOTRTATESFPHPGNNSLPNKDHNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 120
DB 81 EGCOTRTATESFPHPGNNSLPNKDHNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 140
QY 121 SCLISGSGSTSSPOLRLPHTLRCAANTITIEHQKCEANYPGNTIDTMVCASVQEGGKDSQC 180
DB 141 SCLISGSGSTSSPOLRLPHTLRCAANTITIEHQKCEANYPGNTIDTMVCASVQEGGKDSQC 200
QY 181 GDSGGPLVCNOSLGGIISWGDPCAITRKPGVYTKCKYVDMIOETMKNN 230
DB 201 GDSGGPLVCNOSLGGIISWGDPCAITRKPGVYTKCKYVDMIOETMKNN 250

RESULT 7
ABB95526
ID ABB95526 standard; Protein; 250 AA.
XX
AC ABB95526;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiomy; cytoskeletal; antiangiogenic; hypotensive; vulnery;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN MO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219555P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806869.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.

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```

XX (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERB/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PAON/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WJ, Ye W;
XX WPI: 2002-171999/22.
DR N-PSDB; ABL95664.
XX
PS Claim 11; Fig 208; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
SO Sequence 250 AA;
XX
Query Match 100.0%; Score 1263; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIITGFECKRHSOPWQALFEKTRLLCGATLIPRMLTAAHCLKPRYTHLQOHNLQKE 60
DB 21 RIITGFECKRHSOPWQALFEKTRLLCGATLIPRMLTAAHCLKPRYTHLQOHNLQKE 80
QY 61 EGCOTRTATESFPHPGNNSLPNKDHNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 120
DB 81 EGCOTRTATESFPHPGNNSLPNKDHNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 140
QY 121 SCLISGSGSTSSPOLRLPHTLRCAANTITIEHQKCEANYPGNTIDTMVCASVQEGGKDSQC 180
DB 141 SCLISGSGSTSSPOLRLPHTLRCAANTITIEHQKCEANYPGNTIDTMVCASVQEGGKDSQC 200
QY 181 GDSGGPLVCNOSLGGIISWGDPCAITRKPGVYTKCKYVDMIOETMKNN 230
DB 201 GDSGGPLVCNOSLGGIISWGDPCAITRKPGVYTKCKYVDMIOETMKNN 250

RESULT 8
ABB84920
ID ABB84920 standard; Protein; 250 AA.
XX
AC ABB84920;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1279 protein sequence SEQ ID NO: 208.
XX

```


KM Human; angiogenesis; cardiant; cyostatic; antiangiogenic; hypotensive;
 KM vulnereary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KM age-related macular degeneration; arterial restenosis; angina;
 KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KM wound healing; chromosome mapping; gene mapping.
 OS Homo sapiens.
 XX WO20020690-A2.
 XX 03-JAN-2002.
 XX 20-JUN-2001; 2001WO-US19692.
 XX 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220644P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0766498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerlitsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 XX WPI; 2002-090516/12.
 DR N-PSDB; ABL88175.
 DR
 XX
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 XX Claim 11; Fig 208; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cyostatic,
 CC antiangiogenic, hypotensive, vulnereary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides
 CC proteins, agonists and antagonists are useful for treating or diagnosing

CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1263; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-113;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIIRGFECRPHSOPWQAAIFKTRLLCGATLTAARWLLTAHCKLPRIYHGLGHNLOKE 60
 DB 21 RIIRGFECRPHSOPWQAAIFKTRLLCGATLTAARWLLTAHCKLPRIYHGLGHNLOKE 80
 QY 61 EGCQTRTATESPFPHPFNNSLPNKHNDIMLVKMA SPVITWAVRPLTSSRCYTAGT 120
 DB 81 EGCQTRTATESPFPHPFNNSLPNKHNDIMLVKMA SPVITWAVRPLTSSRCYTAGT 140
 QY 121 SCLISGWSTSSPOLRLPHRLRCANITLIEHQKCNAPGNTIDPMVCASVOEGKDSQC 180
 DB 141 SCLISGWSTSSPOLRLPHRLRCANITLIEHQKCNAPGNTIDPMVCASVOEGKDSQC 200
 QY 181 GDGSGPLVCNOSLQGIISWQDPCATIRKRGVYTKVKYDWDIETMKN 230
 DB 201 GDGSGPLVCNOSLQGIISWQDPCATIRKRGVYTKVKYDWDIETMKN 250
 RESULT 9
 ID AUB83684 standard; Protein: 250 AA.
 XX AUB83684;
 AC AAU83684;
 XX 08-MAY-2002 (first entry)
 DT
 XX
 DE Human PRO protein, Seq ID No 186.
 XX
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KM breast cancer; prostate tumour; rectal tumour; liver tumour;
 KM pericyte cell proliferation; chondrocyte cell proliferation;
 KM tumour necrosis factor-alpha.
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 PD 31-JAN-2002.
 XX
 XX 29-JUN-2001; 2001WO-US21066.
 PF
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23322.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.

PR	20-DEC-2000;	200MWO-US34956.
PR	28-FEB-2001;	2001MO-US06520.
PR	10-MAY-2001;	2001US-0854280.
PR	25-MAY-2001;	2001MO-US17092.
XX		
PA	(GETH) GENENTECH INC.	
PI	Baker KP, Deansoyers L, Gerritsen ME, Goddard A, Godowski PJ;	
PI	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;	
XX		
DR	WPI: 2002-172001/72.	
XX	N-PsDB: ABR33628.	
PT		
PT	One hundred and twenty two nucleic acids encoding PRO polypeptides,	
PT	useful for treating a PRO related disorder and for diagnosing tumours	
PT	such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal	
PT	tumour or liver tumour -	
XX		
PS	Claim 11; Figure 186; 359pp; English.	
XX		
CC	The invention relates to one hundred and twenty two nucleic acids	
CC	encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides	
CC	encode human secreted proteins. The PRO nucleic acids, polypeptides,	
CC	agonists and antagonists are useful for treating a PRO related disorder.	
CC	The PRO polypeptides are useful for diagnosing tumours, especially lung	
CC	cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or	
CC	liver tumour. The PRO polypeptides are useful for stimulating the	
CC	proliferation of, or gene expression, in pericyte cells, for stimulating	
CC	the proliferation or differentiation of chondrocyte cells, for	
CC	stimulating the release of tumour necrosis factor-alpha from human blood,	
CC	for stimulating or inhibiting the proliferation of normal human dermal	
CC	fibroblast cells. The PRO polypeptide may also be used as molecular	
CC	weight markers and for tissue typing. The PRO nucleic acids have	
CC	applications in molecular biology, including use as hybridisation probes,	
CC	and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO	
CC	protein sequences of the invention.	
XX		
SQ	Sequence 250 AA:	
	Query Match 100.0%; Score 1263; DB 23; Length 250;	
	Best Local Similarity 100.0%; Pred. No. 2e-113;	
	Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 RIIRFECKRPHQPOMALFEKTRLLCGATLLAPRRULLTAARHLAKRYIVHLCQHNLQKE 60	
Db	21 RIIRKEECKRPHQPOMAALEFKTRLLCGATLLAARRULLTAARHLAKRYIVHLCQHNLQKE 80	
OY	61 EGCEDTFRATESFFPPGFENNSLPNKRHRNDIMLVKMAVSVSTIWAVRPLTLSSRCYTACT 120	
Db	81 EGCEDTFRATESFFPPGFENNSLPNKRHRNDIMLVKMAVSVSTIWAVRPLTLSSRCYTACT 140	
OY	121 SCLISGWGSTSPQLRLPHTLRCANITIIIEHKCENAYNGINTDTMYCASVDEGGKDSQC 180	
Db	141 SCLISGWGSTSPQLRLPHTLRCANITIIIEHKCENAYNGINTDTMYCASVDEGGKDSQC 200	
OY	181 GDSGGPLVCNOSLOGIISWGDPICALTRRGVYTKYCKVDVMTQEFMKNN 230	
Db	201 GDSGGPLVCNOSLOGIISWGDPICALTRRGVYTKYCKVDVMTQEFMKNN 250	
RESULT 10		
ID	AAV42439	
XX	AAV42439 standard; Protein; 282 AA.	
AC	AAV42439;	
XX		
DT	08-DEC-1999 (first entry)	
XX		
DE	CASB12 amino acid sequence.	
KW	neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;	
KW	autoimmune disease.	

OS	Homo sapiens.
XX	
PN	W09949055-A1.
XX	
PD	30-SEP-1999.
XX	
PF	17-MAR-1999; 99WO-EP01894.
XX	
XX	20-MAR-1998; 98GB-0006095.
PA	(SMIK) SMTTHKLINB BEECHAM BIOLOGICALS.
XX	
P1	Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;
XX	
DR	WPI; 1999-580450/49.
DR	N-PSDB; AAZ22638.
PT	New human serine protease CASB12, for treatment, prevention and
XX	diagnosis of cancer and autoimmune diseases
PS	Claim 3; Page 48; 58pp; English.
XX	
CC	This is the amino acid sequence of the CASB12 protein. The nucleotide
CC	sequence of AAZ22638 shows homology with neuropilin and the encoded
CC	protein AAZ22638, is structurally related to other proteins of the
CC	serine protease family, having homology and/or structural similarity
CC	with neuropilin. It is expected that as well as similar structure, these
CC	proteins will also share similar biological functions and properties.
CC	The CASB12 polypeptides and polynucleotides can be used to develop
CC	methods for identifying agonists and antagonists/inhibitors of these
CC	molecules, and thereby treating conditions associated with CASB12
CC	polypeptide imbalance. The invention also provides for diagnostic assays
CC	for detecting diseases associated with inappropriate CASB12 polypeptide
CC	activity or levels.
CC	Since CASB12 is either specifically expressed or highly over-expressed
CC	in tumors compared to normal cells, the polypeptides and polynucleotides
CC	of the invention are believed to be important immunogens for specific
CC	prophylactic or therapeutic immunization against tumors. The
CC	polypeptides and polynucleotides can therefore be targeted by antigen
CC	specific immune reactions (which result in the destruction of the tumor
CC	cell) or they can be used to diagnose the occurrence of tumor cells
SQ	
	Sequence 282 AA;
	Query Match 100.0%; Score 1263; DB 20; Length 282;
	Best Local Similarity 100.0%; Pred. No. 2,4e-113;
	Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 RIRKFECKPHOPOMALFEKTRILCGTLTAPRMLTFAHCLPRYVHIGOHNTLKE 60
Db	53 RIRKFECKPHOPOMALFEKTRILCGTLTAPRMLTFAHCLPRYVHIGOHNTLKE 112
OY	61 ECCEOTRTATESFPHPGFENSLPKNRDHRNDIMLVKMAFVSITMAVRPLTSSRCTACT 120
Db	113 ECCEOTRTATESFPHPGFENSLPKNRDHRNDIMLVKMAFVSITMAVRPLTSSRCTACT 172
OY	121 SCLISGWSSTSPOLRLHTLTLCANITTIIEHOKCENAYPGNTIDPMVCASVOEGKDSQ 180
Db	173 SCLISGWSSTSPOLRLHTLTLCANITTIIEHOKCENAYPGNTIDPMVCASVOEGKDSQ 232
OY	181 GDSGGPLVCNOSLGIIISWGDDPCAITRKPGVYTVCKXYVDIIOETMNN 230
Db	233 GDSGGPLVCNOSLGIIISWGDDPCAITRKPGVYTVCKXYVDIIOETMNN 282
RESULT 11	
AAB11712	
ID	AAB11712 standard; Protein: 282 AA.
AC	AAB11712;
XX	
XT	23-OCT-2000 (first entry)

FT /note- "this corresponding residue in PSA is
 FT involved in intramolecular disulphide bond
 FT
 FT Modified-site 222
 FT /note- "potential casein kinase II phosphorylation site"
 FT Active-site 229..240
 FT /note- "serine protease trypsin family active site motif"
 FT Misc-difference 223
 FT /note- "the corresponding residue (together with
 FT Ser235, Gly252 and Gly263) in neuropsin
 FT forms a oxyanion hole"
 FT Disulfide-bond 231
 FT /note- "this corresponding residue in PSA is
 FT involved in intramolecular disulphide bond
 FT formation"
 FT Misc-difference 235
 FT /note- "the corresponding residue (together with
 FT Asp229, Gly252 and Gly263) in neuropsin
 FT forms a oxyanion hole"
 FT Misc-difference 235
 FT /note- "this forms the active site catalytic triad
 FT with His94 and Asp142"
 FT Disulfide-bond 241
 FT /note- "this corresponding residue in PSA is
 FT involved in intramolecular disulphide bond
 FT formation"
 FT Modified-site 242
 FT /note- "potential N-glycosylation site"
 FT Misc-difference 252
 FT /note- "the corresponding residue (together with
 FT Asp229, Ser235 and Gly263) in neuropsin
 FT forms a oxyanion hole"
 FT Disulfide-bond 256
 FT /note- "this corresponding residue in PSA is
 FT involved in intramolecular disulphide bond
 FT formation"
 FT Modified-site 259
 FT /note- "potential protein kinase C phosphorylation site"
 FT Misc-difference 263
 FT /note- "the corresponding residue (together with
 FT Asp229, Ser235 and Gly252) in neuropsin
 FT forms a oxyanion hole"
 FT Modified-site 278
 FT /note- "potential protein kinase C phosphorylation site"
 FT
 FT W09941387-A2.
 FT
 FT 19-AUG-1999.
 FT
 FT PD 05-FEB-1999: 99WO-US02571.
 FT
 FT PR 17-FEB-1998: 98US-0025059.
 FT
 FT PA (INCY-) INCYTE PHARM INC.
 FT
 FT PI Tang YT, Corley NC, Guegler KJ;
 FT
 FT DR WPI: 2000-012993/01.
 FT
 FT DR N-PSDB: AAZ30222.
 FT
 FT PT New prostate-associated serum protease and polynucleotides which
 FT identify and encode PRASP, useful for treating reproductive disorders
 FT and cancer
 FT
 FT PT
 FT
 FT PS Claim 1; Fig 1A-D; 67pp; English.
 FT
 FT CC The present sequence represents human prostate-associated serum protease
 CC (PRASP). The protein shows homology to neuropsin, a brain-specific
 CC protease in mice, and PSA, a prostate-specific protease in humans.
 CC Nucleic acids encoding PRASP were first identified in incyte clone
 CC 2723646 from the lung tumour cDNA library. Pharmaceutical compositions
 CC containing PRASP, or antibodies to PRASP, and mimetics, agonists,
 CC antagonists or inhibitors of PRASP, are used for treating or preventing

CC a reproductive disorder or cancer. Examples of reproductive disorder
 CC include, abnormal prolactin production, infertility, tubal disease,
 CC ovulatory defects, endometriosis, polycystic ovary syndrome, autoimmune
 CC disorders, ectopic pregnancy, breast cancer, abnormal spermatogenesis
 CC and testicular cancer. Examples of cancers which may be treated or
 CC prevented include adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder,
 CC bone, bone marrow, brain, breast, cervix, penis, prostate, salivary
 CC glands, skin, spleen, testis, thymus, thyroid and uterus. A vector
 CC capable of expressing PRASP or an agonist which modulates the activity of
 CC PRASP may be administered to treat or prevent a reproductive disorder or
 CC cancer.
 CC
 CC SQ Sequence 282 AA:
 CC
 CC Query Match 100.0%; Score 1263; DB 21; Length 282;
 CC Best Local Similarity 100.0%; Pred. No. 2, 4e-113;
 CC Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 RIIRGFECKRHSQPMQALFEKTRLLCGATLIPRMLTFAHCLKPRYIVHLOHNLQKE 60
 CC |
 CC Db 53 RIIRGFECKRHSQPMQALFEKTRLLCGATLIPRMLTFAHCLKPRYIVHLOHNLQKE 112
 CC
 CC QY 61 ECGEQRTATRESPPHGFNNSLPKKDRNDIMLYKASPVSTIWAYRPLTSSRCYTAGT 120
 CC |
 CC Db 113 ECGEQRTATRESPPHGFNNSLPKKDRNDIMLYKASPVSTIWAYRPLTSSRCYTAGT 172
 CC
 CC QY 121 SCLISGWTSSPOLRLPHRLRCANITIIHOKCENAYPGNTIDTMYCASVQEGKDSQC 180
 CC |
 CC Db 173 SCLISGWTSSPOLRLPHRLRCANITIIHOKCENAYPGNTIDTMYCASVQEGKDSQC 232
 CC
 CC QY 181 GDSGGPLVCNQSLOGIISWGDCPCATYRKPGVYTKCKYVDWIOETKNN 230
 CC |
 CC Db 233 GDSGGPLVCNQSLOGIISWGDCPCATYRKPGVYTKCKYVDWIOETKNN 282
 CC
 CC RESULT 13
 CC AAY42440
 CC ID AAY42440 standard; Protein; 281 AA.
 CC
 CC AC AAY42440;
 CC
 CC DT 08-DEC-1999 (first entry)
 CC
 CC DE CASB12 polypeptide derived from Expressed Sequence Tag products.
 CC
 CC XX neuropsin; cancer; assay; inhibitor; serine protease; immunogenic;
 CC KM autoimmune disease.
 CC
 CC OS Homo sapiens.
 CC
 CC XX
 CC PN W09949055-A1.
 CC
 CC PD 30-SEP-1999.
 CC
 CC PF 17-MAR-1999: 99WO-EP01894.
 CC
 CC PR 20-MAR-1998: 98GB-0006095.
 CC
 CC XX
 CC PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 CC
 CC PI Bruck CEM, Cassart J, Coche T, Vinals-bassols C;
 CC
 CC DR WPI: 1999-580450/49.
 CC
 CC DR N-PSDB: AAZ22639.
 CC
 CC PT New human serine protease CASB12, for treatment, prevention and
 CC diagnosis of cancer and autoimmune diseases
 CC
 CC PS Claim 27; Page 49-50; 58pp; English.
 CC
 CC XX This is the amino acid sequence of CASB12 protein, derived from an
 CC Expressed Sequence Tag (EST) search for tumor-specific and

CC tumor-associated antigens. The nucleotide sequence of AA222638 shows
 CC homology with neuropilin and the encoded protein AAV42439 is structurally
 CC related to other proteins of the serine protease family, having homology
 CC and/or structural similarity with neuropilin. It is expected that as well
 CC as similar structure, these proteins will also share similar biological
 CC functions and properties.
 CC The CASB12 polypeptides and polynucleotides can be used to develop
 CC methods for identifying agonists and antagonists/inhibitors of these
 CC molecules, and thereby treating conditions associated with CASB12
 CC polypeptide imbalance. The invention also provides for diagnostic assays
 CC for detecting diseases associated with inappropriate CASB12 polypeptide
 CC activity or levels.
 CC Since CASB12 is either specifically expressed or highly over-expressed
 CC in tumors compared to normal cells, the polypeptides and polynucleotides
 CC of the invention are believed to be important immunogens for specific
 CC prophylactic or therapeutic immunization against tumors. The
 CC polypeptides and polynucleotides can therefore be targeted by antigen
 CC specific immune reactions (which result in the destruction of the tumor
 CC cell) or they can be used to diagnose the occurrence of tumor cells

SO Sequence 281 AA:

Query Match 99.5%; Score 1257; DB 20; Length 281;
 Best Local Similarity 100.0%; Pred. No. 8,9e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIIGFECKPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIYHLCGHNLQKE 60
 DB 53 RIIGFECKPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIYHLCGHNLQKE 112
 QY 61 EGCQRTATSEPPHGFNNSLPNKDRNDIMLVKMASPVSTIWAVRPLTSSRCVTAGT 120
 DB 113 EGCQRTATSEPPHGFNNSLPNKDRNDIMLVKMASPVSTIWAVRPLTSSRCVTAGT 172
 QY 121 SCLISGSGSSSPQLRLPHRLRCANITIIHOKCENAYPENGITDTMWCASVOEGSKSCQ 180
 DB 173 SCLISGSGSSSPQLRLPHRLRCANITIIHOKCENAYPENGITDTMWCASVOEGSKSCQ 232
 QY 181 GDSGGLVNCQSLQGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 229
 DB 233 GDSGGLVNCQSLQGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 281

RESULT 14
 AAB11714
 ID AAB11714 standard; Protein; 275 AA.
 AC AAB11714;
 DT 23-OCT-2000 (first entry)
 DE Human serine protease BSSP6 (hbSSP6) SMQ ID NO:6.
 KW BSSP6; serine protease; human; hbSSP6; mouse; mbSSP6; brain;
 KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
 KW epilepsy; cancer; inflammation; infertility; pancreatitis;
 KW prostatic hypertrophy.
 OS Homo sapiens.
 PN WO200031257-A1.
 PD 02-JUN-2000.
 PF 19-NOV-1999; 99WO-JP06476.
 PR 20-NOV-1998; 98JP-0347802.
 PA (FUSO) FUSO PHARM IND LTD.
 PI Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsui S;
 DR WPI; 2000-40067/34.

DR N-PSDB; AAA61765.
 XX Serine protease BSSP6, useful in detecting homologs, mutants and
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
 PT using blood or other tissues
 PS Claim 15; Page 77-78; 94pp; Japanese.
 XX The invention relates to novel serine proteases designated BSSP6
 CC (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-A61765).
 CC The invention also relates to vectors and transformants comprising BSSP6
 CC nucleic acids; transgenic animals in which the expression level of BSSP6
 CC can be varied; and an mbSSP6 knockout mouse. The invention additionally
 CC encompasses anti-BSSP6 antibodies and methods of production of such
 CC antibodies, methods of BSSP6 detection using the antibodies, and the
 CC use of BSSP6 proteins or fragments as diagnostic markers for certain
 CC medical conditions. Nucleotides encoding BSSP6 were initially
 CC isolated in a human brain cDNA library using degenerate PCR primers
 CC (AAA61795-A61796) based on conserved regions of serine proteases. The
 CC BSSP6 serine proteases and nucleotides encoding them are useful in
 CC detecting homologues, mutants and polymorphic variants in biological
 CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
 CC and spleen) as diagnostic markers for conditions such as Alzheimer's
 CC disease, epilepsy, cancer, inflammation, infertility and prostatic
 CC hypertrophy. Sequences AAB11712 and AAB11714 represent human BSSP6
 CC variants (hbSSP6), and sequence AAB11713 represents murine BSSP6
 CC (mbSSP6).

SO Sequence 275 AA:

Query Match 98.2%; Score 1240.5; DB 21; Length 275;
 Best Local Similarity 90.2%; Pred. No. 3,4e-111;
 Matches 230; Conservative 0; Mismatches 0; Indels 25; Gaps 1;

QY 1 RIIGFECKPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIYHLCGHNLQKE 46
 DB 21 RIIGFECKPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIYHLCGHNLQKE 80
 QY 47 -----RYIVHLCGHNLQKEGCEQRTATSEPPHGFNNSLPNKDRNDIMLVK 95
 DB 81 SSSNYCLSHLSRYIVHLCGHNLQKEGCEQRTATSEPPHGFNNSLPNKDRNDIMLVK 140
 QY 96 MASPVSTIWAVRPLTSSRCVTAGTSCGISGWSSTSPQLRLPHRLRCANITIIHOKCE 155
 DB 141 MASPVSTIWAVRPLTSSRCVTAGTSCGISGWSSTSPQLRLPHRLRCANITIIHOKCE 200
 QY 156 NAYPGNITDTMWCASVOEGKSCQSDSGGLVNCQSLQGIISWGODPCATIRKPGVYTK 215
 DB 201 NAYPGNITDTMWCASVOEGKSCQSDSGGLVNCQSLQGIISWGODPCATIRKPGVYTK 260
 QY 216 VCKYVDWIOETMKN 230
 DB 261 VCKYVDWIOETMKN 275

RESULT 15
 AAB21312
 ID AAB21312 standard; Protein; 228 AA.
 AC AAB21312;
 DT 02-FEB-2001 (first entry)
 DE Human TLSP.
 KW Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; TLSP;
 KW trypsin-like serine protease; kallikrein-like protein; serine protease;
 KW cytosolic; cancer; prostrate cancer.
 OS Homo sapiens.
 PN WO200053776-A2.

```
XX 14-SEP-2000
PD
XX
XX 09-MAR-2000; 2000MO-CA00258.
PF
XX
XX 11-MAR-1999; 99US-0124260.
PR
XX 01-APR-1999; 99US-0127386.
PR
XX 21-JUL-1999; 99US-0144919.
XX
PA (MOUN ) MOUNT SINAI HOSPITAL.
XX
XX Yusef GM, Diamandis EP;
PI
XX
XX WPI; 2000-567440/55.
DR
XX
XX
XX New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
PT protein mediated disorders, especially cancer.
XX
XX
XX Example 3; Fig 9; 184pp; English.
PS
XX
XX The present sequence is human trypsin-like serine protease (TLSP), a
CC member of the kallikrein multi-gene family. Kallikreins and
CC kallikrein-like proteins are a subgroup of the serine protease enzyme
CC family. They catalyze the selective cleavage of specific polypeptide
CC precursors to release peptides with potent biological activity. Nucleic
CC acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4,
CC KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the
CC treatment, monitoring and diagnosis of cancers, especially prostate
CC cancer. They can also be used to identify a substance that can associate
CC with or mediate the biological activity of the proteins. Antibodies can
CC be used to treat conditions mediated by the kallikrein-like proteins.
XX
SQ Sequence 228 AA;
Query Match 97.9%; Score 1236; DB 21; Length 228;
Best Local Similarity 100.0%; Pred. No. 7.2e-111;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RITKGFECKPHSQPQNALFEKTRLLCGATLLPRLMTAHCCKPRYIVHGLQHNLQKE 60
DB 4 RITKGFECKPHSQPQNALFEKTRLLCGATLLPRLMTAHCCKPRYIVHGLQHNLQKE 63
QY 61 EGCQOTRTATESPFPFGFNNSLPNKDRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 120
DB 64 EGCQOTRTATESPFPFGFNNSLPNKDRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGT 123
QY 121 SCLISGSGSTSSPQLRLPHTLRCANITIIIEHOKCENAYPGNITDTMWCVASVQEGKDSQ 180
DB 124 SCLISGSGSTSSPQLRLPHTLRCANITIIIEHOKCENAYPGNITDTMWCVASVQEGKDSQ 183
QY 181 GDSGGPLVNCOSLQGIISWGQPCATTRKPGYTKCKYVDWIQE 225
DB 184 GDSGGPLVNCOSLQGIISWGQPCATTRKPGYTKCKYVDWIQE 228
```

Search completed: December 23, 2002, 14:19:06
Job time : 81 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2002, 14:21:47 ; Search time 2231 Seconds
(without alignments)
1669,638 Million cell updates/sec

Title: US-09-856-320a-2_COPY_53_282
Perfect score: 1263
Sequence: 1 RIITGFECKPHSQPMQALF.....GVYTKCKVYDWIQETMKN 230

Scoring table:
BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xip
-O=/cgr2_1/USPTO.spool/US09856320/runat_23122002_113712_22707/app_query.fasta_1.391
-DB=EST -OPMT=fastlap -SUFFIX=est -MINMATCH=0.1 -LOOPT=0.0 -LOOEXT=0.0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09856320 -CGCN_1_1_2024_@runat_23122002_113712_22707 -NCPU=6 -ICPU=3
-NO_XLPYX -NO_MMV -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-YARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estda:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_estc3:*
13: gb_estc4:*
14: gb_estc5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	1228.5	97.3	1294	11 BC015551	BC015551 Homo sapi
2	1158	91.7	841	13 B1818697	B1818697 603037514
3	1146	90.7	678	13 B1763040	B1763040 603047836
4	1146	90.7	833	12 BG120793	BG120793 602692015
5	1117.5	88.5	1072	13 BM559782	BM559782 AGENCOURT
6	1067	84.5	1295	11 AK009360	AK009360 Mus muscu
7	1067	84.5	1295	11 AK009720	AK009720 Mus muscu
8	1066.5	84.4	1074	13 BM559617	BM559617 AGENCOURT
9	1041	82.4	1269	11 AK009659	AK009659 Mus muscu
10	963	76.2	708	12 BG697071	BG697071 602660281
11	857	67.9	639	12 BG747134	BG747134 602704354
12	793.5	62.8	973	12 BE867930	BE867930 601443517
13	780	61.8	761	14 BM982377	BM982377 UT-CE-EN1
14	724	57.3	467	9 A1893370	A1893370 mJ99H09.Y
15	720	57.0	467	9 AA073833	AA073833 mJ99H09.Y
16	669	53.0	539	14 BM837078	BM837078 K-EST0113
17	632	50.0	1048	11 AK004807	AK004807 Mus muscu
18	628.5	49.8	1240	11 AK003996	AK003996 Mus muscu
19	620.5	49.1	368	9 AA412318	AA412318 zB97C06.T
20	607	48.1	451	14 W60374	W60374 zB97C06.T
21	605	47.9	754	13 B163899	B163899 603280742
22	599.5	47.5	890	11 AK009217	AK009217 Mus muscu
23	591	46.8	394	11 BE150851	BE150851 RC4-HT027
24	590	46.7	799	11 AK007843	AK007843 Mus muscu
25	589	46.6	799	11 AK008660	AK008660 Mus muscu
26	589	46.6	802	11 AK008667	AK008667 Mus muscu
27	589	46.6	802	11 AK003064	AK003064 Mus muscu
28	587	46.5	956	12 BF164946	BF164946 601778180
29	577	45.7	759	13 BJ502684	BJ502684 Mus muscu
30	573	45.4	815	11 AK003082	AK003082 Mus muscu
31	571.5	45.2	877	11 AK002278	AK002278 Mus muscu
32	567	44.9	904	13 B1759204	B1759204 603042631
33	567	44.9	1051	13 BM547198	BM547198 AGENCOURT
34	565.5	44.8	820	12 BG688173	BG688173 602187278
35	565	44.7	809	12 BF679282	BF679282 602153475
36	564.5	44.7	856	11 AK007406	AK007406 Mus muscu
37	562.5	44.5	759	9 A1326340	A1326340 mJ61608.X
38	561.5	44.5	760	12 BF538381	BF538381 602053872
39	561.5	44.5	860	12 BG868885	BG868885 602784464
40	561	44.4	733	12 BG270402	BG270402 1b14603.Y
41	556.5	44.1	582	10 AM243944	AM243944 xO91B07.X
42	556.5	44.1	808	13 BM438186	BM438186 IDLVR0020
43	556	44.0	734	12 BG270328	BG270328 1b13605.Y
44	553.5	43.8	827	12 BG685835	BG685835 602788248
45	553	43.8	870	11 AK007773	AK007773 Mus muscu

ALIGNMENTS

RESULT 1
BC015551
LOCUS BC015551 1294 bp mRNA linear HTC 29-OCT-2001
DEFINITION Homo sapiens, kallikrein 11, clone IMAGE:3847555, mRNA.
ACCESSION BC015551
VERSION BC015551.1 GI:15930236
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1294)
AUTHORS Strausberg, R.
TITLES Direct Submission
JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian

REMARK
COMMENT

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdpaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 20 Row: 1 Column: 12
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA 91: 8574438
 This clone has the following problem: frame shifted.

FEATURES

source

Location/Qualifiers
 1..1294
 /organism="Homo sapiens"
 /db_xref="locusid:11012"
 /db_xref="taxon:9606"
 /clone="IMAGE:3847565"
 /tissue_type="Colon, adenocarcinoma"
 /clone_lib="NIH_MGC_65"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6"
 /note="Vector: PCMV-SPORT6"

BASE COUNT 317 a 391 c 334 g 252 t
 ORIGIN

Alignment Scores:

Pred. No.: 1,69e-120 Length: 1294
 Score: 1228.50 Matches: 229
 Percent Similarity: 99.14% Conservative: 1
 Best Local Similarity: 98.71% Mismatches: 0
 Query Match: 97.27% Indels: 2
 DB: 11 Gaps: 1

US-09-856-320A-2_COPY_53_282 (1-230) x BC015551 (1-1294)

QY 1 Arg11e1le1y1p1h1e1g1u1c1y1s1p1r1o1h1s1e1r1g1n1p1r1o1t1r1p1a1a1a1e1u1p1h1e 20
 |||||||
 Db 275 AGGATATCAAGGGGTTGAGTGCACAGCCCTACTCCAGCCCTGGCAGGAGCCCTGTTTC 334
 QY 21 G1u1y1t1h1r1a1r1e1u1e1u1c1y1a1a1a1h1r1e1u1l1e1a1p1r1o1r1g1r1p1e1u1r1h1a1a 40
 : : : : :
 Db 335 AAGAAACGCGGCTACTGCTGTGGGCGAGCCTCATGCCGCCAGATGGCTCTGACAGCA 394
 QY 41 Ala1h1s1c1y1e1u1p1r1o1h1s1e1r1g1n1p1r1o1t1r1p1a1a1a1e1u1p1h1e 59
 |||||||
 Db 395 GCGCCACTGGCTCAAGCGCGTGCCTACATAGTTCACCTGGGCGACACCAACTCCAGAA 454
 QY 59 s1g1u1g1a1s1p1e1r1g1y1p1r1o1e1u1a1l1e1h1a1r1g1y1s1p1r1o1h1s1e1r1g1n1p1r1o1t1r1p1a1a 79
 |||||||
 Db 455 GGGAGAGGCGCTGTGACAGACCGGACAGCCTGAGTCTTCCGCCACCCGGCTTCAA 514
 QY 79 na1s1e1r1e1u1p1r1o1h1s1e1r1g1n1p1r1o1t1r1p1a1a1a1e1u1p1h1e 99
 |||||||
 Db 515 CAACACCTCCCAACAAAGACACCGCATATGATCATCTGCTGTAAGATGCGATCGCC 574
 QY 99 o1a1l1s1e1r1e1u1p1r1o1h1s1e1r1g1n1p1r1o1t1r1p1a1a1a1e1u1p1h1e 119
 |||||||
 Db 575 AGTCTCATCACTCGGCTGTGCGACCCCTCACCTCTCTCCAGCTGTCTCACTCTCG 634
 QY 119 y1h1s1e1r1e1u1p1r1o1h1s1e1r1g1n1p1r1o1t1r1p1a1a1a1e1u1p1h1e 139
 |||||||
 Db 635 CACGACCTGCTCATTTCCGGCTGGGCGACGACGCTCAGCCCATTTACGCTTGCCTCA 694

QY 139 s1h1r1e1u1a1r1g1c1y1a1a1a1n1l1e1h1r1l1e1g1u1h1s1g1n1y1c1y1s1g1u1a1n1a1t1y1r1p1 159
 |||||||
 Db 695 CACCTTGCATGCGCCACATCACTATTCAGCCACGAGATGTGAGAAACCCCTACCC 754
 QY 159 o1g1a1n1l1e1h1r1a1p1h1e1t1a1l1c1y1a1s1e1r1a1l1e1h1a1r1g1y1s1p1r1o1h1s1e1r1g1n1p1r1o1t1r1p1a1a 179
 |||||||
 Db 755 CGGCACATCAACAGACACCACTGTGTGTCCACAGTGCAGAGAGGGGCAAGACCTCTG 814
 QY 179 s1c1u1g1a1s1p1e1r1g1y1p1r1o1e1u1a1l1e1h1a1r1g1y1s1p1r1o1h1s1e1r1g1n1p1r1o1t1r1p1a1a 199
 |||||||
 Db 815 CCAAGGAGTACCGGGGGCCCTGTGCTGTATACAGTCTCTTCAAGCATTTATCTCCG 874
 QY 199 p1g1y1a1s1p1r1o1c1y1a1a1l1e1h1a1r1g1y1s1p1r1o1h1s1e1r1g1n1p1r1o1t1r1p1a1a1a1e1u1p1h1e 219
 |||||||
 Db 875 GGGCCAGATCCCTGTGCTGTACCCGAAAGCCCTGTGTCTACAGAAAGTGTCAATA 934
 QY 219 r1a1a1s1p1r1i1e1g1u1h1r1e1t1y1a1s1n1a1s1n 230
 |||||||
 Db 935 TGTGACTGTGATCCAGAGACGATGAAGACAAAT 968

RESULT 2
 B1818697
 LOCUS
 DEFINITION B1818697 841 bp mRNA linear EST 04-OCT-2001
 603037514F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178746 5',
 mRNA sequence.
 ACCESSION B1818697
 VERSION B1818697.1 GI:15930247
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L14M1445. row: k column: 03
 High quality sequence stop: 784.

FEATURES

source

Location/Qualifiers
 1..841
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5178746"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

BASE COUNT 180 a 288 c 206 g 167 t
 ORIGIN

Alignment Scores:

Pred. No.: 2.92e-113 Length: 841
 Score: 1158.00 Matches: 222
 Percent Similarity: 97.38% Conservative: 1
 Best Local Similarity: 96.94% Mismatches: 5
 Query Match: 91.69% Indels: 5

DB: 13 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x B1818697 (1-841)

QY 7 GLUCYASyProHISserGln-ProTrpGlnAlaIleuPhegluYrThrArgLeu 26
|||||
Db 2 GAGGACAGCCCTCACCTCCAGTCCCTGGCAGGACCCCTGTCCAGAAAGCGGCTACT 61

QY 26 UCYSgLYAlaThrLeuIleAlaProArgTrpLeuThrAlaAlaHIScysLeuSpr 46
|||||
Db 62 CTGGGGGGCAGCTCATCCGCCAGATGGCTCTCAGACAGACCCACTGCTCAAGCC 121

QY 46 OArgTrpIleValHISleuGlyGlnHISAsnLeuGlnGlyGluGlycysGluGlnThr 66
|||||
Db 122 CCCTATAGTATGATTCACCTGGGGCAGCACAACTCCAGAGAGAGGGCTGTGAGCAGAC 181

QY 66 rArg-THrAlaThrGlnSerPheProHISProGlyPheAsnAsnSerLeuProAsnLys 86
|||||
Db 182 CTGGAGAGCCAGCTGAGTCTCCGCCACCCCGCTTCAACACAGCTCCCAACAAAG 241

QY 86 sPHISArgAsnAPILeMetLeuValLysMetAlaSerProValSer-IleThrTrpAla 105
|||||
Db 242 ACCACGCCAATGACATATGCTGTGTAAGATGGCATGGCATGCTCTATCAGCTGGGCT 301

QY 106 ValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSer 125
|||||
Db 302 GTGGGACCCCTCACCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361

QY 126 GLYTrpGlySerThrSerSerProGlnLeuArgLeuProHISThrLeuArgCysAlaAsn 145
|||||
Db 362 GGGGGGGGAGCAGTCCAGCCGCCAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421

QY 146 IleThrIleIleGlnHISGlnLysCysGluAsnAlaIleThrProGlyAsnIleThrAspThr 165
|||||
Db 422 ATCACCATCTTGAGCAGCAGAAAGTGTGAGAAAGCCCTACCCGCAACATCAGAGAACCC 481

QY 166 MetValCysAlaSerValGlnGlu-GlyGlyLysAspSerCysGlnLysAspSerGly 185
|||||
Db 482 ATGTGTGTCTCCAGCTGAGCAGGAGGGGCAAGGAGTCTCTGCAAGGAGTCTCCGAGG 541

QY 185 YProLeuValCysAsnGlnSerLeuGln-GlyIleIleSerTrpGlyGlnAspProCys 205
|||||
Db 542 CCCTGGCTGTGTACAGTCTCTCAATGCAATATCTCTGGGGCAGAGTCCGCTG 601

QY 205 IAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAspTrpIleGln 225
|||||
Db 602 CGATACACCCGAAAGCTGTGTCTACACGAAAGTCTGCAATATGTGAGTGTGATCCAG 661

QY 225 IuThrMetLysAsnAsn 230
|||||
Db 662 AGACGATGAAGAACAT 678

RESULT 3
B1763040 678 bp mRNA linear EST 25-SEP-2001
LOCUS B1763040
DEFINITION 603047836F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187896 5',
mRNA sequence.
ACCESSION B1763040
VERSION B1763040.1 GI:15754618
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 678)
REFERENCE NIH-MGC <http://imgc.ncl.nih.gov/>
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL1469 row: h column: 09
High quality sequence stop: 647.
Location/Qualifiers
1. 678
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5187896"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; site:1: NotI, site:2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

BASE COUNT 152 a 234 c 172 g 120 t
ORIGIN

Alignment Scores:
Pred. No.: 3 97e-112 Length: 678
Score: 1146.00 Matches: 210
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 1
Query Match: 90.74% Indels: 0
DB: 13 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x B1763040 (1-678)

QY 20 PheGluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThr 39
|||||
Db 10 TTGAGAAAGAGGGGGCTACTGCTGGGGCAGCCTCATCCGCCAGATGGCTCTGACA 69

QY 40 AlAlaHIScysLeuLysProArgTrpIleValHISleuGlyGlnHISAsnLeuGlnLys 59
|||||
Db 70 GCAGCCACAGTCTCAAGCCCGCTACATGATTCACCTGGGGCAGCAGCACTCCAGAA 129

QY 60 GluGluGlycysGluGlnThrArgTrpAlaThrGlnSerPheProHISProGlyPheAsn 79
|||||
Db 130 GAGGAGGGCTGTAGCAGACCCGAGCAGCCATGAGTCTTCCCAACCCCGGCTTCAAC 189

QY 80 AsnSerLeuProAsnLysAspHISArgAsnAPILeMetLeuValLysMetAlaSerPro 99
|||||
Db 190 AACAGCTCCCAACAAAGCAGCAGCGAATGATCATGCTGTGTAAGATGGCATGCCCA 249

QY 100 ValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGly 119
|||||
Db 250 GTCTCATCATCCTGGGGCTGTGACACCCCTCTCCACAGCTGTGTCTGCTGCTGCTGCT 309

QY 120 ThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHIS 139
|||||
Db 310 ACCAGCTGCTCATTTCCGCTGGGGCAGCAGTCCAGCCCGAGTTCAGCTGTGCTGCTGCT 369

QY 140 ThrLeuArgCysAlaAsnIleThrIleGlnHISGlnLysCysGluAsnAlaIleTrpPro 159
|||||
Db 370 ACCTTGAGATGGCCCAACATCAGCATATGAGCAGACAGAAAGTGAAGAGGCTTACCC 429

QY 160 GlyAsnIleThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCys 179
|||||
Db 430 GGCACATCATCAGACACCAATGAGTGTGCCAGCTCAGAAAGGGGCAAGGAGCTCTCC 489

QY 180 GluGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp 199
|||||
Db 490 CAGGTGACTCTCGGGGGCCCTGTGCTGTATACCAAGTCTTCAAGGCAATTATCTCTGG 549

QY 200 GYGLNAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyr 219
 DB 550 GGCAGGATCCGTGTCGATCAAGCCGAGGCTGCTACAGAAAGTGTGCAATAT 609
 QY 220 ValAspTPIleGlnGlnThrMetLysAsnAsn 230
 DB 610 GTGGACTGGATCCAGAGCAGTGAAGAACAT 642

RESULT 4
 BG720793 853 bp mRNA linear EST 08-MAY-2001
 LOCUS 602692015F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4824387 5',
 DEFINITION mRNA sequence.
 ACCESSION BG720793
 VERSION BG720793.1 GI:13999980
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 1 (bases 1 to 853)
 NIH-MGC http://mhc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihaki
 Toshiyuki and Piero Carninci (RIKEN)
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 cDNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10735 row: n column: 04
 High quality sequence stop: 826.

FEATURES
 Source
 1. 853
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4824387"
 /clone_11b="NIH_MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
 size-selected for average insert size 2.2 kb and
 normalized for ROP 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NHGRI/NHGRI, National
 Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 180 a 285 c 227 g 161 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5.72e-112 Length: 853
 Score: 1146.00 Matches: 217
 Percent Similarity: 98.19% Conservative: 0
 Best Local Similarity: 98.19% Mismatches: 3
 Query Match: 90.74% Indels: 2
 DB: 12 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x BG720793 (1-853)

QY 1 ArgIleIleLysGlyPheGlnLysProHisSerGlnProTrglnAlaAlaLeuPhe 20
 DB 193 AGGATCATCAAGGGGTTCAGGTCAAGCTCCACGCTGCGAGGACCCCTGTTC 252

QY 21 GlnLysThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 40
 DB 253 GAGAGAGCGCGGCTACTCTGTGGGGCGAGCTATCGCCCAAGATGGTCTGTGACAGA 312

QY 41 AlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
 DB 313 GCCATGCTCATTAAGGCCCGGCTACATAGTTCACTGTGGGCGACACCAACTCCAGAAAGGAG 372

QY 61 GlnGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProLysPheAsnAsn 80
 DB 373 GAGGGGTGTGACAGACCCGAGACGACTGATCTTCCCGGAGCCCGGCTTCAACAAC 432

QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetLysSerProVal 100
 DB 433 AGCTGCTCATTAATTCGGGCGGAGACGCTCCAGCCCGGCTTCAACAAC 492

QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
 DB 493 TCCATTCACCTGGGCTGTGTGACCCCTCCTCTCTCAGCTGTGTCACTGTGGACAC 552

QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
 DB 553 AGCTGCTCATTAATTCGGGCGGAGACGCTCCAGCCCGGCTTCAACAAC 612

QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGly 160
 DB 613 TTGGCATGGCCCAACATCAATCAATTCATGAGACCAAGATGTGAGAGACCCGCTACCCGGC 672

QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
 DB 673 AACATTCACAGACCATGGTGTGTGACAGCTGACAGAGGGGGGCAAGCATCTGTCCAG 732

QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpL 200
 DB 733 TT-GACTCCGGGGGCTCTGTGTGTGTACCAAGTCTTCAAGGCAATTAATCTCCGGCT 791

QY 200 yGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyr 220
 DB 792 GCAGATTCGCTGTGATACCCGGAAGCTGTGTCTACAGAAAGTGTGCAATATGT 851

QY 220 1 220
 DB 852 G 852

RESULT 5
 BM559782 1072 bp mRNA linear EST 20-FEB-2002
 LOCUS 6565460 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5744410
 DEFINITION 5', mRNA sequence.
 ACCESSION BM559782
 VERSION BM559782.1 GI:18803655
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 1 (bases 1 to 1072)
 NIH-MGC http://mhc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM12765 row: 1 column: 11
 High quality sequence stop: 684.

FEATURES
 Source
 1. 1072
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5744410"
 /clone_11b="NIH_MGC_119"

/tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: PCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH-MGC library."

BASE COUNT 238 a 340 c 307 g 185 t 2 others
 ORIGIN

Alignment Scores:

Score: 1117.50 length: 1072
 Percent Similarity: 95.56% Matches: 213
 Best Local Similarity: 94.67% Mismatches: 7
 Query Match: 88.48% Indels: 3
 DB: 13 Gaps: 1

US-09-856-320a-2_copy_53_282 (1-230) x BM559782 (1-1072)

QY 1 Argillelelysglypheglucyslyspromisserglnprotrpglnalalauphe 20
 Db 272 AGGATCATCAAGGGGTTGAGTGCAGCCCTCCAGCCCTGCGAGGAGCCCTGTC 331
 QY 21 GlulysThrargyleuleucysglyAlaThrleuileAlaProargtrpleuThrAla 40
 Db 332 GAGAAAGCGGGGCTACTCTGGGGCGACCTCTACCCCAATAGGCTCTGACAGCA 391
 QY 41 AlahiscysleuysproargtyrileValhiscylnglnhinsanleuglnlysglu 60
 Db 392 GCCCAGCTCCCAAGCCCGCTACATAGTTCACCTGGGCGAGCAGCAACCTCCAGAGAG 451
 QY 61 GlulyscysgluInThrargThrAlaThrGluSerPheProhispProglyPheAsn 80
 Db 452 GAGGGCTGTAGCAGACCCCGACAGCCACGACGCTTCCCGCCAGCCGCTTCAACAC 511
 QY 81 SerleuproasnlyspasphissargspasplleuMetleuVallysmetAlaserProval 100
 Db 512 AGCTCCCAAGAGCCACCGCATGATCATCTGTGTGAGAGGATGCGATCCAGTC 571
 QY 101 SerleThrtrpAlaValArgProleuThrleuSerSerArgcysValThrAlaGlyThr 120
 Db 572 TCCATACCCGNGCTGTGGCAGCCCTCACCCTCCCTGCTGTCTGCTGCTGCGAC 631
 QY 121 SerCysleuileserglytrpglySerThrSerSerProglInleuArgleuProhispThr 140
 Db 632 AGCTGCTCATTTCCGGCTGGGCGAGCAGCTCCAGCCCGAGTTACGCTGCCACAC 691
 QY 141 LeuArgysAlaAsnleThrlelleleGlnhiscylnglnyscysgluAsnAlaTyProgly 160
 Db 692 TTGGATGCGCCCAACATCCATCATGACACACAGAAAGTGTGAAGCGCTACCCCGG 751
 QY 161 AsnleThrAspThrmetValcysAlaserValGlnGlnGlylylyAspSerCysGln 180
 Db 752 CACATCAACACACATGAGTGTGGCCAGCGTGCAGAGAGGGGCGACAGCATCTCGNCA 811
 QY 181 GlyAspSerGlyProleuValcysAsnGlnSerleuGlnGlylelleSerTrpgly 200
 Db 812 GGGAGACCCCGGGGCGCTGTGTGTGAACAGCTCTTCAAGGCATTAATCTCGGGC 871
 QY 201 -GlnAspProCysAlaAlaThrarglyspProglyValTyThr---TyValCyslysty 219
 Db 872 CCGAGATCCGCTGTGCGATCCCGGAAAGCGCTGTGTCTACCGGAAAGGTCTGCGATA 931
 QY 219 rVal-AspTrp 222
 Db 932 TGTGGGACTGG 942
 RESULT 6

AK009360

LOCUS

DEFINITION

AK009360 1295 bp mRNA linear HTC 19-JAN-2002
 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015108:protease, serine, 20, full insert sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

5 (bases 1 to 1295)
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arikawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Haneoka, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hirooka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,

MEDLINE
 PUBMED
 99279253
 10349636
 REFERENCE
 AUTHORS
 TITLE
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

JOURNAL
 MEDLINE
 PUBMED
 20499374
 11042159
 REFERENCE
 AUTHORS
 TITLE
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Sumi, H., Akiyama, T., Nishik, K., Kitanai, T., Tashiro, H., Itoh, M., Konno, H., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaiguchi, S., Ikegami, T., Kasaiyagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

JOURNAL
 MEDLINE
 PUBMED
 20530913
 11076861
 REFERENCE
 AUTHORS
 TITLE
 4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Salto, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Salto, R., Kadote, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, D., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, T., Pesole, G., Quackenbush, J., Schriml, L. M., Staib, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Bader, L., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamly, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Togo-Oka, K., Wang, K. H., Weitz, C., Willeker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kotsuki, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection. *Nature* 409 (6821), 685-690 (2001)

JOURNAL
 MEDLINE
 PUBMED
 21085660
 11217851
 REFERENCE
 AUTHORS
 TITLE
 5 (bases 1 to 1269)
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hangaki, T., Hara, A., Hayatsu, N., Hill, D., Yamamoto, K., Hirakawa, T., Horii, F., Hume, D., Imoto, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Konda, M., Koya, S., Kunita, C., Matsuyama, T., Miyazaki, A., Nishik, K., Nomura, K., Numata, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tezuka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission

TITLE
 JOURNAL
 Direct Submission
 Physical and Chemical Research (RIKEN). Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Shuto-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
 Please visit our web site (http://genome-gsc.riken.go.jp/) for further details.
 cDNA library was prepared and sequenced in Mouse Genome

	Enyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGACAAAGATCCAGACGCTCTCTTTTCTTTTTTCTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAAGAGAGACTTCCTCAGGTAAATTAAATATATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI, 3' end: SstI. Host: SOLR.					
FEATURES						
source	Location/Qualifiers					
	1..1269					
	/organism="Mus musculus"					
	/strain="C57BL/6J"					
	/db_xref="FANTOM.DB:2310037E23"					
	/db_xref="MGI:1894042"					
	/db_xref="taxon:10090"					
	/clone="2310037E23"					
	/sex="male"					
	/tissue_type="tongue"					
	/clone_lib="RIKEN full-length enriched mouse cDNA library"					
	/dev_stage="adult"					
	1..1269					
misc_feature	/note="data source:MGI, source key:MGI:1929977, evidence:ISS protease::serine_20" /db_xref="MGI:1929977"					
BASE COUNT	307 a 363 c 304 g 295 t					
ORIGIN						
Alignment Scores:						
Pred. No.:	1 79e-100 Length: 1269					
Score:	1041.00 Matches: 186					
Percent Similarity:	91.30% Conservative: 24					
Best Local Similarity:	80.87% Mismatches: 20					
Query Match:	82.42% Indels: 1					
DB:	11 gaps: 0					
US-09-856 -320A-2_COPY_53_282 (1-230) x AK009659 (1-1269)						
OY	1 Argillelelysglypheglucyslyspbrohisserginprotprginalaleupehe 20					
Db	AGGATCATCAAGGGGTATAGTAGTGCGAGGCCCTCACAGGCATGGCAGGTGGCCCTTTT 316					
OY	21 GlulystrhratrgleuleucysglyAlathrleullealaprroarqtrpleuleuthrAla 40					
Db	CAGAAGACACCGCTTCCTGTGGGGGCAACCCTCATCGCCCCCAAATGGCTTCGACAGCA 376					
OY	41 AlaHscyleuleuspProtoargtyrlilValAlHstlenuglgnHisAnleuinGlunly6lu 60					
Db	GCCCCACCTGCGCCAGAGCCCATTAAGTGTCTCTCTTGGAGAGCCAAATCTPAGAGAACACA 436					
OY	61 GluglcysgluglnInthrArgThrAlaThrcLusSerPheProHisProglYpheaAsn 80					
Db	GACGGCTGTGAGCGAGG-CGGATGGCCACGTAGAGCTCTTCCGCCACCCGACTTCACACAC 495					
OY	81 SerleupProasnlysaSPHisArGaAsnaspIlleMetLeuVallySMetaLSerProval 100					
Db	AGCCTCCCCAACAAAGACACACCGGAATGACATAATGCTTGGAGAGATGTGTCTCCGCTC 555					
OY	101 SerlierhrtpAlaValAngProleuthrLeuSerSerArGcysValThrAlaglyThr 120					
Db	TTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 615					
OY	121 SerCysleuileSerGlyTyPrGLYSerThrsSerSerProGlnleuarGrleuProHIsth 140					
Db	AGCTGCGTCATTTTGTGATGGGACACACAGCTCCAGCCCCAAGTTGGCCCTGCTCATTC C 675					
OY	141 LeuarGcysAlaasnillethrlllelgLnHslnglnScySGluasnaLatyrProglY 160					

Db 676 TTGCGATGTCGAATGCTTCATCATCGAAGACAGAGGTGTGAGAGGCTTACCGGGC 735
 Qy 161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 180
 Db 736 AACATCAGACACATGCTGTCGCGCAGTGTTCGGAAAGAGGCAAGGACTCTGTGAC 795
 Qy 181 GLYAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGly 200
 Db 796 GGTGACTGTGGAGGCCCCGCTGCTGCACAGGATCTTCACAGGACATCATCTCTGGGGT 855
 Qy 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
 Db 856 CAGAGCCATGATGCTCCCTGACAGAAAGCCTGGTGTCTATACAAAGTCTGCAATACTTT 915
 Qy 221 AspTyrIleGlnGluThrMetLysAsnAsn 230
 Db 916 AACTGATCCAGAGGTATAGAGAACAT 945

RESULT 10
 LOCUS BG697071 708 bp mRNA linear EST 07-MAY-2001
 DEFINITION 60260281F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:480356 5',
 mRNA sequence.
 ACCESSION BG697071
 VERSION BG697071.1 GI:13962880
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-riemail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10699 row: a column: 21
 High quality sequence stop: 704.

FEATURES
 source
 1..708
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:480356"
 /clone_lib="NCI_CGAP_Skn3"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: skin; Vector: PCMV-SPORE6; Site:1: NCI;
 Site:2: Sall; Cloned unidirectionally. Primer: Oligo df.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 147 a 262 c 183 g 116 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.54e-92 Length: 708
 Score: 963.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 76.25% Indels: 0
 DB: 12 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x BG697071 (1-708)

Qy 1 ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTyrPheGlnAlaLeuPhe 20
 Db 175 AGAGTATCATAGAGGCTTCAGTGCAGAGCTCTACCTCCAGCCCTGGCAGGACCCCTGTTCC 234

Qy 21 GlnLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuThrAla 40
 Db 235 GAGAAAGCGGGCTACTGTGTGGGCGAGCGCTATCGCCCGCAGATGGCTCTGACAGCA 294
 Qy 41 AlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
 Db 295 GCCACTGGCTCAAGCCCCGCTACATATGTCACCTGGGCGAGACAACTCCAGAGGAG 354
 Qy 61 GlnGlyCysGlnGlnThrArgThrAlaThrGlnLysSerPheProHisProGlyPheAsn 80
 Db 355 GAGGGGTGTGAGAGAGACCGGAGAGCAGCTAGTACTCTTCCCGCCCGGCTTCAACAC 414
 Qy 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
 Db 415 AGCCTCCCAACAAAGACCCGCAATGACATCATCTGCTGTGAGATGTCATCGCAGTTC 474
 Qy 101 SerIleThrAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
 Db 475 TCCATCACCCTGGGCTGTGTGACCCCTGACCTCTCTCTCAGCTGTCTACTCTGGCACC 534
 Qy 121 SerCysLeuIleSerGlyTyrPylSerThrSerSerProGlnLeuArgLeuProHisThr 140
 Db 535 AGTGCGCTATTTCCGGCTGGGGGCGAGCAGTCCAGCCCACTTACGCTCTCAGACC 594
 Qy 141 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGly 160
 Db 595 TTGCGATGCGCCACATCATCATTTGAGCAGACAGAAAGTGTAGAACCCCTTACCCGGC 654
 Qy 161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAsp 177
 Db 655 AACATCAGACACCATGCTGTGTGCGCAGCTGACAGAGGGGCGCAAGGAC 705

RESULT 11
 LOCUS BG747134 639 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602704354F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:485773 5',
 mRNA sequence.
 ACCESSION BG747134
 VERSION BG747134.1 GI:14057787
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-riemail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM1710 row: k column: 14
 High quality sequence stop: 638.

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:485773"
 /clone_lib="NIH_MGC_15"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: colon; Vector: pOTR7; Site:1: XhoI; Site:2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 128 a 241 c 162 g 108 t
ORIGIN

Alignment Scores:

Pred. No.: 2,79e-81 Length: 639
Score: 857.00 Matches: 157
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.37% Mismatches: 0
Query Match: 67.85% Indels: 0
DB: 12 Caps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x BE8747134 (1-639)

QY 1 ArgillelelysglypneglucysalysProhisserglnProtrpglnAlaAlaLeuPhe 20
DB 165 AGGATCATCAAGGGGTTGAGTGCAGGCTCACCAGCCCTGGACGAGCCCTGTTC 224
QY 21 GlulysThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTTPLeuLeuThrAla 40
DB 225 AAGAAGACGGCGCTACTCTGTGGGGCGACGCTCATCGCCCAAGATGGCTCTGACAGCA 284
QY 41 AlaHisCysleuLysProArgTyrIleValHisIleuGlyGlnHisAsnLeuGlnLysGlu 60
DB 285 GCCCACTGCTCAAGCCCGCTACATAGTTACCTGGGGACGACAACTTCACAGAGAG 344
QY 61 GlulysCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 80
DB 345 GAGGCGTGTAGACAGACCCGACAGCCAGCTAGTCCTCCCAACCCCGGCTTACAGAC 404
QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
DB 405 AGCTCTCCCAAGAAAGACCCGCAATGACATGCTGTGGAGAGATGGATCCGCCAGTC 464
QY 101 SerIleThrPalaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
DB 465 TCCATTCACCTGGGCTGTGGCAGCCCTCACCCTCTCTCACCCTGTGTACGTGGGACC 524
QY 121 SerCysLeuIleSerGlyTTPGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
DB 525 AGCTGCCATCTTCGGCTGGGGGACAGCAGTCACGCCCGGTTACGCTGCCACAGCC 584
QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyr 158
DB 585 TTGGATGCGGCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAGAACGGCTTAC 638

RESULT 12
BE867930 973 bp mRNA linear EST 20-OCT-2000

DEFINITION 601443517F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847565 5',
mRNA sequence.

ACCESSION BE867930
VERSION BE867930.1 GI:10316706
KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 973)

NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: ceabs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

plate: LHAM562 row: a column: 06

High quality sequence stop: 714.

Location/Qualifiers

FEATURES

source

1..973

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3847565"

/clone_1db="NIH_MGC_65"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: Vector: pcMV-SPORE6; Site:1: NotI;

Site:2: SalI; Cloned unidirectionally. Primer: oligo dT.

Average insert size 1.8 kb. Library constructed by Life

Technologies.

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DEFINITION UI-CF-EN1-acs-o-17-0-UI-s1 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-acs-o-17-0-UI-s1', mRNA sequence.
 ACCESSION BM982377
 VERSION BM982377.1 GI:19605813
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 761)
 AUTHORS Bonaldi,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704447
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA
 sequence: 17-100, >LINE2 (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
 source
 Location/Qualifiers
 1..761
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-CF-EN1-acs-o-17-0-UI"
 /clone_1lb="UI-CF-EN1"
 /tissue_type="Primary Lung Cystic Fibrosis Epithelial
 Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-CF-EN1 is a normalized cDNA library containing the
 following tissue(s): Primary Lung Cystic Fibrosis
 Epithelial Cells. The library was constructed according to
 Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was ligated to an EcoR I adaptor, digested with Not
 I, and cloned directionally into pT73-Pac vector. The
 oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CAGCTCAGGT.
 TAG_L1B=UI-CF-EN1
 TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
 6hr to LPS 24h
 TAG_SEQ=CTGCTCAGGT"
 BASE COUNT 172 a 170 c 222 g 195 t 2 others
 ORIGIN

Alignment Scores:
 Pred. No.: 6.25e-73 Length: 761
 Score: 780.00 Matches: 143
 Percent Similarity: 99.31% Conservative: 0
 Best Local Similarity: 99.31% Mismatches: 1
 Query Match: 61.76% Indels: 0
 DB: 14 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x BM982377 (1-761)

QY 87 HisArgAsnApIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaVal 106
 |||||
 Db 761 CACCGCATGATCATCATGCTGTGMAAGATGATCGCATCGCATCTCCATCCACTGGCTGTG 702
 QY 107 ArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGly 126
 |||||
 Db 701 CGACCCCTCACCCCTCTCTCTACAGTGTGTCATGCTGGCAGCCAGCTGCTCATTTCCGCCG 642
 QY 127 TrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIle 146
 |||||
 Db 641 TGGGGCAGCAGCGTCAGCCGCCAGTTAGCGCTGCTCACACCTTGGAGTGGCCACATC 582
 QY 147 ThrIleIleGlnHisGlnLysCysGluAsnAlaTyr-ProGlyAsnIleThrAspThrMet 166
 |||||
 Db 581 ACCATCATTTGAGCAGCAGAAAGTGTGAGAACGCCCTACCCGCGCAACATCAGACACCATG 522
 QY 167 ValCysAlaSerValGlnGlnGlnGlyLysAspSerCysGlnGlnLysPserGlyPro 186
 |||||
 Db 521 GTGTGTCCAGCCGTGAGGAAGGGGCGAAGACTCTGCGAGGTAATCCGGGGCCCT 462
 QY 187 LeuValCysAsnGlnSerLeuGlnGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIle 206
 |||||
 Db 461 CTGTGTCTGATCAGCATCTCTTCAAGCATTAATCTCTGGGGCCAGATCCGTGCGATC 402
 QY 207 ThrArgLysProGlyValTyrThrLysValCysLysTyr-ValAspTrpIleGlnIleThr 226
 |||||
 Db 401 ACCGGAAGCGCTGTGTCTACAGAAAGTCTGCAAAATATGTGACTGATTCAGAGAGC 342
 QY 227 MetLysAsnAsn 230
 |||||
 Db 341 ATGAGAGAACAT 330

RESULT 14
 A1893370 467 bp mRNA linear EST 15-MAR-2000
 A1893370
 LOCUS m199h09.y1 Soares mouse p3MWF19.5 Mus musculus cDNA clone
 DEFINITION IMAGE:484289.5 similar to gb:030785 Mouse mRNA for neuropsin, cds
 (MUSE);, mRNA sequence.
 A1893370
 A1893370.1 GI:5599272
 ACCESSION
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 467)
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,T., Person
 ,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 The WashU-NCI Mouse EST Project 1999
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LBNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 Putative full length read
 vector to vector length is 833
 MG1:295033
 Seq primer: -40RP from Gibco
 High quality sequence stop: 445.

FEATURES
 source
 Location/Qualifiers
 1..467
 /organism="Mus musculus"
 /db_xref="taxon:10090"

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 467)	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
1 (bases 1 to 467)	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.	The MashU-HMI Mouse EST Project	Unpublished (1996)	Contact: Marra M/Mouse EST Project MashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LML ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:295033
Seq primer: -28M13 rev2 from Amersham				
High quality sequence stop: 322.				
Location/Qualifiers				
1. .467				
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/clone_id="Soares mouse p3NMF19.5"				
/dev_stage="19.5 dpc total fetus"				
/lab_host="DH10B (ampicillin resistant)"				
/note="Vector: pUT73p (pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5', TGTTACCAATCTGAAGTGGGCGCGGCATTTTCTTTTCTTTT 3'), TGTTACCAATCTGAAGTGGGCGCGGCATTTTCTTTTCTTTT 3'), adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pUT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State university)."				
BASE COUNT	102 a 154 c 114 g 97 t			
ORIGIN				
Alignment Scores:				
Prod. NO.:	7.44e-67	Length:	467	
Score:	720.00	Matches:	130	
Percent Similarity:	91.61%	Conservative:	12	
Best Local Similarity:	83.87%	Mismatches:	13	
Query Match:	57.01%	Indels:	0	
DB:	9	Gaps:	0	
US-09-8556-320A-2_COPY_53_282 (1-230) x AA073833 (1-467)				
0Y 63 CysgluIntrArgThAlaThrCluSerPheProHisProGlyPheAsnAsnSerIeu 82				
Db 3 TGTGCGAGGAGGCGGATGGCCAGTGAAGCTCTTCCGCCACCCGACTTCAACAAACGCCCTC 62				
0Y 83 ProAsnLysASpHisArgAsnAspIleMetIeuValLysMetAlaSerProValSerIle 102				
Db 63 CCCAACAAAGACCCACCGGAATGACATAATGCTGTGGAAGATGTCGTCGCCCTCTTTT 122				
0Y 103 ThrTPAlaValArgProIeuThrLeuSerSerArgCysValThAlaGlyThSerCys 122				
Db 123 ACCGAGCTGTGCAGACCACTCACCCCTGCCCCACACTGTGTGCGTGCAGGACCAAGCTGC 182				
0Y 123 LeuIleSerGlyTTPGlySerThrSerSerProGlnLeuArgIeuProHisThrIeuArg 142				
Db 183 CTCATTTCTGTGATGGGGGACGACGATCCAGGCCGCCAGTTGGCCCTGCATTTCCCTWCGGA 242				
0Y 143 CysAlaAsnIleThrIleIleGluHisGlnIleCysGluAsnAlaTyrProGlyAsnIle 162				
Db 243 TGTGCAATGTCTCATCATTCGAAACACAAAGAGTGTGAGAAAGGCGCTTACCCGGGCAACATTC 302				

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 13:16:17 ; Search time 92 Seconds

(without alignments)
515.118 Million cell updates/sec

Title: us-09-856-320a-2_COPY_53_282

Perfect score: 1263
Sequence: 1 RIILKEFECKRHSQPMQALF.....GVYTKVCKYVDWIQETMKNN 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMEL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1067	84.5	249	11 090YN4	09qyn4 mus musculus
2	1067	84.5	276	11 090YN3	09qyn3 mus musculus
3	681	53.9	255	4 096R00	096r00 homo sapien
4	632	50.0	251	11 09DBQ8	09dbq8 mus musculus
5	628.5	49.8	293	11 09D140	09d140 mus musculus
6	599.5	47.5	234	11 09CV76	09cv76 mus musculus
7	592	46.9	246	11 09Z1R9	09z1r9 mus musculus
8	590	46.7	246	11 090UK9	090uk9 mus musculus
9	589	46.6	246	11 0980T7	0980t7 mus musculus
10	588.5	46.6	239	11 083275	063275 rattus norv
11	587.5	46.4	235	11 063274	063274 rattus norv
12	586.5	46.4	261	11 09JMT0	09jmt0 mus musculus
13	579.5	45.9	261	6 09N101	09n101 saginus oe
14	579.5	45.9	261	6 029474	029474 canis fami
15	565	44.8	251	11 054854	054854 rattus norv
16	565	44.7	249	11 091VE3	091ve3 mus musculus

17	564.5	44.7	247	11 09CPN7	09cpn7 mus musculus
18	563	44.6	262	4 08TCV8	08tcv8 homo sapien
19	562.5	44.5	237	13 091515	091515 fugu rubrip
20	562.5	44.5	244	13 08QGW3	08qgw3 anguilla ja
21	561.5	44.5	263	11 09JMT1	09jmt1 mus musculus
22	559.5	44.3	263	11 09JMT6	09jmt6 mus musculus
23	558.5	44.2	245	13 042160	042160 petromyzon
24	558	44.2	240	13 098TH0	098th0 engraulis j
25	558	44.2	246	11 088301	088301 mus musculus
26	558	44.2	253	11 091Y82	091y82 mus musculus
27	553	43.8	247	11 09CPN9	09cpn9 mus musculus
28	552.5	43.7	244	13 042159	042159 petromyzon
29	552.5	43.7	254	6 09XSN6	09xsn6 sus scrofa
30	551	43.6	238	13 09W706	09w706 paracichthy
31	549.5	43.5	247	13 042158	042158 petromyzon
32	548.5	43.4	247	13 042608	042608 petromyzon
33	548.5	43.4	261	11 088309	088309 mus musculus
34	547	43.3	247	11 09DTY7	09dty7 mus musculus
35	546.5	43.3	242	13 092099	092099 paracichthy
36	543.5	43.0	242	13 09W707	09w707 paracichthy
37	541.5	42.9	242	13 093266	093266 pseudopleur
38	540	42.8	241	13 098RG9	098rg9 engraulis j
39	540	42.8	247	13 09W705	09w705 paracichthy
40	532.5	42.2	249	13 09W6K0	09w6k0 notothenia
41	526.5	41.7	675	13 09W6J8	09w6j8 dissostichu
42	525.5	41.6	255	11 09JIS2	09jis2 mus musculus
43	519.5	41.1	249	13 092046	092046 dissostichu
44	519.5	41.1	255	11 09ZOM1	09zom1 mus musculus
45	503.5	39.9	344	13 09W6J9	09w6j9 dissostichu

ALIGNMENTS

RESULT 1

ID 090YN4 PRELIMINARY; PRT: 249 AA.
AC 090YN4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2002 (TREMBLrel. 20, Last annotation update)
DE HIPPOSTASIN (2310015108RIK protein).
GN PRSS20 OR 2310015108RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Mitsui S., Yamaguchi N.;
RT "cDNA cloning of a novel brain serine protease, Hippostasin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Borrelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA  Gustinich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mondaeris P.,
RA  Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA  Sasaki H., Sato K., Schenbach C., Seta T., Shidara Y., Storch K.,
RA  Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA  Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA  Hayashizaki Y.;
RT  *Functional annotation of a full-length mouse cDNA collection.*;
RL  Nature 409:685-690(2001).
CC  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC  TRYPsin FAMILY.
DR  EMBL: AB016226; BAA88825.1; -.
DR  EMBL: AK009720; BAB26461.1; -.
DR  EMBL: AK009360; BAB26241.1; -.
DR  HSSP: P00763; IDPO.
DR  MEROPS: S01.257; -.
DR  MGd: MGI:1929977; Prss20.
DR  InterPro: IPR001314; Chymotrypsin.
DR  InterPro: IPR001254; Ser_protease_Try.
DR  Pfam: PF00089; Trypsin; 1.
DR  PRINTS: PR00722; CHYMOTRYPsin.
DR  SMART: SM00020; TRYP-Spc; 1.
DR  PROSITE: PS00240; TRYPsin_DOM; 1.
DR  PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR  PROSITE: PS00135; TRYPsin_SER; 1.
DR  Hydrolase: Serine protease.
SQ  SEQUENCE 249 AA; 27604 MW; F9FF9C8457D727D5 CRC64;

Query Match 84.5%; Score 1067; DB 11; Length 249;
Best Local Similarity 81.3%; Pred. No. 1.8e-103;
Matches 187; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 RIKEGECRPHSQPQWALFEKTRLLCGATLLAPRMLLTAHCKRKYVHLCOHNLQKE 60
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QY 61 EGCEQRTATESPFPHPFNNSLPNKHNDIMLVKMASPVSIWAVRPLTSSRCYTAGT 120
DB 80 DGCEQRMATESPFPHPFNNSLPNKHNDIMLVKMASPVSIWAVRPLTSSRCYTAGT 139
QY 121 SCLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDVMCASVQEGKDSQ 180
DB 140 SCLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDVMCASVQEGKDSQ 199
QY 181 GDSGGLVNCNLSQGIISWGDCPCATRKRGVYTKYCKYVDWIOETMKN 230
DB 200 GDSGGLVNCNLSQGIISWGDCPCATRKRGVYTKYCKYVDWIOETMKN 249

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Q90YN3 PRELIMINARY; PRT; 276 AA.
AC Q90YN3;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hipostasin prostate type.
DE PRSS20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RT [2]
RA Tissue cloning and tissue-specific splicing variants of mouse
RT *cDNA cloning and tissue-specific splicing variants of mouse

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RT hipostasin/TISP (PRSS20).";
RL Biochim. Biophys. Acta 1494:206-210(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: AB016227; BAA36955.1; -.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.257; -.
DR MGd: MGI:1929977; Prss20.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPsin.
DR SMART: SM00020; TRYP-Spc; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR Hydrolase: Serine protease.
SQ SEQUENCE 276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;

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Query Match 84.5%; Score 1067; DB 11; Length 276;
Best Local Similarity 81.3%; Pred. No. 2e-103;
Matches 187; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 RIKEGECRPHSQPQWALFEKTRLLCGATLLAPRMLLTAHCKRKYVHLCOHNLQKE 60
DB 47 RIKEGECRPHSQPQWALFEKTRLLCGATLLAPRMLLTAHCKRKYVHLCOHNLQKE 106
QY 61 EGCEQRTATESPFPHPFNNSLPNKHNDIMLVKMASPVSIWAVRPLTSSRCYTAGT 120
DB 107 DGCEQRMATESPFPHPFNNSLPNKHNDIMLVKMASPVSIWAVRPLTSSRCYTAGT 166
QY 121 SCLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDVMCASVQEGKDSQ 180
DB 167 SCLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDVMCASVQEGKDSQ 226
QY 181 GDSGGLVNCNLSQGIISWGDCPCATRKRGVYTKYCKYVDWIOETMKN 230
DB 227 GDSGGLVNCNLSQGIISWGDCPCATRKRGVYTKYCKYVDWIOETMKN 276

```

```

RESULT 3
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AC Q96R00;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Prostloogen.
DE Prostloogen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21226193; PubMed=11327827;
RA Takayama T.K., Carter C.A., Deng T.;
RT *Activation of prostate-specific antigen precursor (pro-PSA) by
RT prostin, a novel human prostatic serine protease identified by
RT RT deenerate PCR.*;
RT Biochemistry 40:1679-1687(2001).
DR EMBL: AF303046; AAK62813.1; -.
DR MEROPS: S01.081; -.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR Hydrolase: Serine protease.
SQ SEQUENCE 255 AA; 27986 MW; 00D5B79E14B9468F CRC64;

Query Match 53.9%; Score 681; DB 4; Length 255;
Best Local Similarity 51.7%; Pred. No. 4.3e-63;
Matches 124; Conservative 36; Mismatches 66; Indels 14; Gaps 3;

```

```

QY 1 RIIFGECKHSPQWQAALEFKTRLLCGATLLIAPRWLLTAHCLKPRYIVHLGQHNLOKE 60
D 20 KLEGGDCACAHSPQWQAALEFKTRLLCGATLLIAPRWLLTAHCLKPRYIVHLGQHNLOKE 79
QY 61 EGCQRTATESPFPHPGPNNSLPKNDHRNDIMLVKMA SPVSIWAVRPLTLSSRCVYAGT 120
D 80 DGEQRLTTRSVTPHPFTE-----AKSHRNDIMLRLVQPARLNDQVPAVLPTRCPHGE 135
QY 121 SCLISGWSGTS-----SP--QLRLPHTLRCANITITIEHOKCENAYPCNITPTMYCAS 170
D 136 ACVYSGMGVLSHNEPGRAGSPRGVSLPDTLHCANIGIISDTSDCKRYPGRILNTWYACAG 195
QY 171 VQESGKDSGCGSGGLVNCOSLOGITISWQDPCATRRKPGVYTKVCKYWDIQTAKNN 230
D 196 AEGRGASGSCGDSGGLVNCOSLOGITISWQDPCATRRKPGVYTKVCKYWDIQTAKNN 255

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RESULT 4

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ID Q9DB08 PRELIMINARY; PRT; 251 AA.
AC Q9DB08;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE 1200016C12Rik protein.
GN 1200016C12Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S., Hill D., Hofmann M., Fujita M., Gariboldi M.,
RA Gustincich S., Hilt D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J.H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL; AK004807; BAB23579.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.307; -.
DR MGD; MGI:1921082; 1200016C12Rik.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYSP-SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 251 AA; 2815 MW; F4D667F8C80C4A23 CRC64;

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Query Match 50.0%; Score 632; DB 11; Length 251;
 Best Local Similarity 51.7%; Pred. No. 5, 6e-58;
 Matches 119; Conservative 37; Mismatches 74; Indels 0; Gaps 0;

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QY 1 RIIFGECKHSPQWQAALEFKTRLLCGATLLIAPRWLLTAHCLKPRYIVHLGQHNLOKE 60
D 22 RAVGARCVCVNSXPWQAGFLYTRQLOGATLLINQWLLTAHCKRPLVWLRGHHLMRW 81
QY 61 EGCQRTATESPFPHPGPNNSLPKNDHRNDIMLVKMA SPVSIWAVRPLTLSSRCVYAGT 120
D 82 EGEQRLTTRSVTPHPFTE-----AKSHRNDIMLRLVQPARLNDQVPAVLPTRCPHGE 141
QY 121 SCLISGWSGTS-----SP--QLRLPHTLRCANITITIEHOKCENAYPCNITPTMYCAS 180
D 142 QCLIFGWSVSSKQYPMTLQCANISILDNKFCRMAYPGHIFKILCAGLWEGGSGSCQ 201
QY 181 GDSGGLVNCOSLOGITISWQDPCATRRKPGVYTKVCKYWDIQTAKNN 230
D 202 GDRGGLVNCOSLOGITISWQDPCATRRKPGVYTKVCKYWDIQTAKNN 251

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RESULT 5

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ID Q9D140 PRELIMINARY; PRT; 293 AA.
AC Q9D140;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE 1110030019Rik protein.
GN 1110030019Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S., Hill D., Hofmann M., Fujita M., Gariboldi M.,
RA Gustincich S., Hilt D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J.H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC EMBL; AK003996; BAB23113.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.418; -.
DR MGD; MGI:1915918; 1110030019Rik.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYSP-SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 293 AA; 31908 MW; ED1F45D8226FE911 CRC64;

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Query Match 49.8%; Score 628.5; DB 11; Length 293;

Best Local Similarity	47.4%	Pred. No. 1.6e-57	Matches 110: Conservative 47: Mismatches 66: Indels 7: Gaps 4
OY	1	R1IKFECKPSPQPOQA-LFEKTLKLCATLITAPRLITAAHCLKPRIVHLLGCHNLOK	59
Db	67	RIVNSDDCKDQAPQWQALLGLPKNLYCGAVLISQWMLTAAHCRPVRIKRGHSMSP	126
OY	60	-EEGQETRTATESPHEGFNSLNPNKHNDIMLVKMASPSTIMAWPLTITSSRCVYA	118
Db	127	YVESQGMFQGIKSLIPHEYS----HFGSNLDMLIKNNKRIRDSHSYKVPVELACDCAIE	182
OY	119	GTSCLSICMGSTSSPOLRLPHTLRCANITITIEHQECENAYPCGNTIDTPYCASVQEGSKDS	178
Db	183	GTRCVSSGGTSSSHNNPKVLQGITINTVLSEERCKNSYPCQIDKTRMCADDEE-GRDS	241
OY	179	CGGDSGGLPVYCNOSLOGIISMGDCGCAITRKGVYTKKCYKYDWOETWKNKNN	230
Db	242	CGGDSGGLPVYCNKGLQGLVSMGDFCAQRNRGVTITNLCEFKWKIKDTMNSN	293
RESULT 6			
O9CV76		PRELIMINARY; PRF: 234 AA.	
AC	O9CV76		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	2310008B01Rik protein (Fragment).		
GN	2310008B01Rik		
OC	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=TONGUE;		
RX	MEDLINE=21085660; PubMed=11217851.		
RA	Kawai J., Shinaagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,		
RA	Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Guernicich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,		
RA	Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cdna collection.";		
RL	Nature 409:665-690(2001).		
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE		
CC	TRYPSIN FAMILY.		
DR	EMBL; AK009217; BAB26143.1; -		
DR	HSSP; P00763; IDPO.		
DR	MEROPS; S01.020; -		
DR	MCD; MGI:1916761; 2310008B01Rik.		
DR	InterPro; IPR001314; Chymotrypsin.		
DR	InterPro; IPR001254; Ser_protease_Try.		
DR	Pfam; PF00089; trypsin.1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	SMART; SMO0020; Tryp_SPC.1.		
DR	PROSITE; PS50240; TRYPSIN_DOM.1.		
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.		
DR	PROSITE; PS00135; TRYPSIN_SER.1.		
TM	Hydrolase; Serine protease.		
TM	NON_TER 1		

Seq	Sequence	234 AA	25888 MW	6081E609EED39110	CRC64
Qy	Query Match	47.5%	Score 599.5	DB 11	Length 234
Db	Best Local Similarity	46.8%	Pred. No. 1.3e-54		
Matches	108	Conservative	40	Mismatches 78	Indels 5
Qy	1 RIRKGECKPHQPOQALFEKTRLLCGATLLAPRLLTAHACLKRPYVHVGQHLQKE 60				
Db	8 KLYNVECKKNQPMQVGLFHGKLYLRGGGVLDVRKRVLVLAANC-RKLYVRRLGEHSLTFL 66				
Qy	61 EECGEOTRATESFPHFGNNLSLPNKDRNDIMLVKMASFVSITWAVRPLTLSRCVTAGT 120				
Db	67 DWTEQLRHTTFESITPHSYGAYON--HEHDLRLRLNRPDIHILTRAVRPAALPSSCWTGTA 124				
Qy	121 SOLGISMGSTSPQRLPPTLRCAANTTIEHCKCEAAYGNTIDPWVCASVQEGGDSQO 180				
Db	125 MCHVSGMGTTNKPMDPFPRRLQCLNLSTVSNETCAVFPGRVETNNLCAG-GEAGDACAQ 183				
Qy	181 GDSGPELVCSNLSGGIISNGQ-DPCAITRRKPGVYTRKCYKVDWIDQETMKN 230				
Db	184 GDSGPELVCSNLSGGIISNGQ-DPCAITRRKPGVYTRKCYKVDWIDQETMKN 234				
RESULT 7					
ID	Q9ZIR9	PRELIMINARY	PRT	246 AA	
AC	Q9ZIR9				
DT	01-MAY-1999 (TREMBLrel. 10, Created)				
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)				
DE	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	Trypsinogen 16.				
GN	TRYGN16 OR TRYPSINOGEN.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BALB/C;				
RA	Rowen L., Hood L.;				
RT	"Comparison between strains Balb/C and 129 in a region of the mouse T cell receptor beta locus."				
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BALB/C;				
RX	MEDLINE=21103195; PubMed=11160223;				
RA	Chen F., Rowen L., Hood L., Rothenberg E.V.;				
RT	"Differential transcriptional regulation of individual TCR vbeta segments before gene rearrangement."				
RL	J. Immunol. 166:1771-1780(2001).				
CC	-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, ALSO KNOWN AS THE TRYPSIN FAMILY.				
DR	EMBL: AF107342; AAC79093.1; -				
DR	EMBL: AE000665; AAB69088.1; -				
DR	HSSP; P00763; IDPO.				
DR	MEROPS; S01.063; -				
DR	MCD; MGI:2148749; Trygn16.				
DR	InterPro: IPR001314; Chymotrypsin.				
DR	InterPro: IPR001254; Ser.protease_Try.				
DR	Pfam: PF00089; trypsin.1				
DR	PRINTS; PR00722; CHYMOTRYPIN.				
DR	SMART; SM00200; TRYP_Spc.1.				
DR	PROSITE; PS50240; TRYPSIN_DOM.1.				
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.				
DR	PROSITE; PS00135; TRYPSIN_SER.1.				
DR	Hydrolase; Serine protease.				
SQ	SEQUENCE 246 AA; 26134 MW; 34E173B18CA2F463 CRC64;				
Query Match	46.9%	Score 592	DB 11	Length 246	
Best Local Similarity	49.6%	Pred. NO. 8.4e-54			
Matches 114	Conservative 33	Mismatches 77	Indels 6	Gaps 3	


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QY 1 RIINGFECKRHSQWQALAEKTLILGATLILAPRMLITAAHCLKPRYIYHLOGHNLQKE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 KIVGGYTCRENSIPYQVSL-NSGYHFCGSLINDQWVVAHACHYKTRIOVRLGHEHNINVL 81
QY 61 EGCQOTRATESPFPHPGNNSLPKKDHNDIMLVKMAFPSITWAVRPLTSSRCVYAGT 120
   || || || || || || || || || || || || || || || || || || || || || ||
Db 82 EGNQOFIDAKIKIHPNFNSKRTLN----NDIMLKISSPYTLNARVATVALPSSCAPAGT 137
QY 121 SCLISGWSSTSSPOLRLPHTLRCANITITIEHOKCENAYPGNITPDWVCASVOEGKDSQC 180
   || || || || || || || || || || || || || || || || || || || || || ||
Db 138 QCLISGNGNTLSFGVSRPDLQCLDAPLLPQADCEASYPKRTNNMIVGLEGKDSQC 197
QY 181 GDSCGPLVCNOSLOGIISWGDPCATIRKPGCVYTKVCKYVDIQTAKNN 230
   || || || || || || || || || || || || || || || || || || || || || ||
Db 198 GDSCGPLVCNGLQIVSGWYG-CALPDNPGVYTKVCNYVDIQTIAAN 246

RESULT 8
Q90UK9 PRELIMINARY; PRT; 246 AA.
ID Q90UK9;
AC Q90UK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE TSP4 (0910001B19RIK protein) (trypsinogen 9).
GN TC OR 0910001B19RIK OR TRYPSINOGEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RC MEDLINE=99436155; PubMed=10506205;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glisli C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderas P., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carrincci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guslinich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RC MEDLINE=2103195; PubMed=1160223;
RA Chen F., Rowen L., Hood L., Rothenberg E.V.;
RT "Differential transcriptional regulation of individual TCR Vbeta
RT segments before gene rearrangement.";
RL J. Immunol. 166:1771-1780(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.

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DR EMBL; AB009661; BAA85187.1; -.
DR EMBL; AB017031; BAA74760.1; -.
DR EMBL; AK007843; BAB25300.1; -.
DR EMBL; AE000664; AAB69057.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.058; -.
DR MGD; MGI:1913350; 0910001B19RIK.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPE; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease.
SQ SEQUENCE 246 AA; 26277 MW; 915C92353EC42809 CRC64;

Query Match 46.7%; Score 590; DB 11; Length 246;
Best local similarity 48.7%; Pred. No. 1.4e-53;
Matches 112; Conservative 36; Mismatches 76; Indels 6; Gaps 3;

QY 1 RIINGFECKRHSQWQALAEKTLILGATLILAPRMLITAAHCLKPRYIYHLOGHNLQKE 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 KIVGGYTCRENSIPYQVSL-NSGYHFCGSLINDQWVVAHACHYKTRIOVRLGHEHNINVL 81
QY 61 EGCQOTRATESPFPHPGNNSLPKKDHNDIMLVKMAFPSITWAVRPLTSSRCVYAGT 120
   || || || || || || || || || || || || || || || || || || || || || ||
Db 82 EGNQOFVNSAKIKIHPNFNSKRTLN----NDIMLKISSPYTLNARVATVALPSSCAPAGT 137
QY 121 SCLISGWSSTSSPOLRLPHTLRCANITITIEHOKCENAYPGNITPDWVCASVOEGKDSQC 180
   || || || || || || || || || || || || || || || || || || || || || ||
Db 138 QCLISGNGNTLSFGVNNPDLQCLDAPLLPQADCEASYPKRTNNMIVGLEGKDSQC 197
QY 181 GDSCGPLVCNOSLOGIISWGDPCATIRKPGCVYTKVCKYVDIQTAKNN 230
   || || || || || || || || || || || || || || || || || || || || || ||
Db 198 GDSCGPLVCNGLQIVSGWYG-CALPDNPGVYTKVCNYVDIQTIAAN 246

RESULT 9
Q9ROT7 PRELIMINARY; PRT; 246 AA.
ID Q9ROT7;
AC Q9ROT7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE TSP4 (0910001B19RIK protein) (trypsinogen 9).
GN TC OR 0910001B19RIK OR TRYPSINOGEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVJ;
RC MEDLINE=99436155; PubMed=10506205;
RA Ohmura K., Kohno N., Kobayashi Y., Yamagata K., Sato S.,
RA Kashiwabara S., Baba T.;
RT "A homologue of pancreatic trypsin is localized in the acrosome of
RT mammalian sperm and is released during acrosome reaction.";
RL J. Biol. Chem. 274:29426-29432(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH AND SPLEEN;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glisli C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

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RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Sessa T., Shidada Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 RL [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=21103195; PubMed=11160223;
 RA Chen F., Rowen L., Hood L., Rothenberg E.V.;
 RT "differential transcriptional regulation of individual TCR beta
 RT segments before gene rearrangement."
 RL J. Immunol. 166:1771-1780(2001).
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: AB017032; BAA74761.1; -;
 DR EMBL: AK008667; BAB25821.1; -;
 DR EMBL: AK003064; BAB2542.1; -;
 DR EMBL: AE000664; AAB69056.1; -;
 DR HSSP: P00763; 1SLU.
 DR MEROPS: S01.057; -;
 DR MGD: MG1:1913350; 0910001B19RLK.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRY-SPC; 1.
 DR PROSITE: PS00134; TRYPSIN_DOM; 1.
 DR PROSITE: PS00135; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydrolyase; Serine protease.
 KW SEQUENCE 246 AA; 26274 MW; B6A9FAC9079633F CRC64;
 SQ
 Query Match 46.6%; Score 589; DB 11; Length 246;
 Best Local Similarity 48.7%; Pred. No. 1.7e-53;
 Matches 112; Conservative 35; Mismatches 77; Indels 6; Gaps 3;
 QY 1 RIKEGFECKPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCKRPYIVHGOHMOKE 60
 DB 23 KIYGVGTCHRENSVYQVSL-NSGYHRCGSLINDQVNSAHCYKSRIGVRLGEHNIIVL 81
 QY 61 ECEQOTRTATESPFRHGFENNSLPKNDHRDMLVKMASPVSTIWAAPLTLSSRCTACT 120
 DB 82 ENEQGVNSAKTIKHPNFNSRLN---NDIMLIKLASVPTLNARVATALPSSCAPAGT 137
 QY 121 SCLISGWSSTSPQLRPLPTLRCANITTEHOKCENAYPGNTIDFWCASVOEGGDSQO 180
 DB 138 QCLISGWSSTSPQLRPLPTLRCANITTEHOKCENAYPGNTIDFWCASVOEGGDSQO 197
 QY 181 GDSGSGPLVNCOSLQGIISWGODPCATTRKPGVYTKVCKYVDIMQETMKN 230
 DB 198 GDSGSGPLVNCOSLQGIISWGODPCATTRKPGVYTKVCKYVDIMQETMKN 246
 RESULT 10
 Q63275 PRELIMINARY; PRT; 239 AA.
 AC Q63275;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Kallikrein (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SUBMANDIBULAR GLAND;
 RA Zintz C.B., Ma J.-X., Chao J., Chao L.;
 RT "Isolation and characterization of a new rat kallikrein cDNA with
 RT predominant expression in the kidney."
 RL Submitted (JAN-1995) to the EMBL/Genbank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: U3840; AA58782.1; -;
 DR HSSP: P00759; 1TON.
 DR MEROPS: S01.411; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRY-SPC; 1.
 DR PROSITE: PS00134; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydrolyase; Serine protease.
 KW NON_TER 1
 KW SEQUENCE 239 AA; 26382 MW; 3CBD761AF06AB53 CRC64;
 SQ
 Query Match 46.6%; Score 588.5; DB 11; Length 239;
 Best Local Similarity 44.9%; Pred. No. 1.9e-53;
 Matches 106; Conservative 46; Mismatches 73; Indels 11; Gaps 3;
 QY 1 RIKEGFECKPHSOPWQALFEKTRLLCGATLLAPRWLLTAHCKRPYIVHGOHMOKE 60
 DB 8 RVYGFCKENKSNOPWQAVINED--LCGVLLDPSVITTAHCHYSDNHYVLLGNNLSLED 65
 QY 61 ECEQOTRTATESPFRHGF-----NNSLPKNDHRDMLVKMASPVSTIWAAPLTLSSR 114
 DB 66 ---VQRLVYSGSPRHPDYKPLMRNTRKPKYSDNMLHLHSEPADITDGVKVIDLPK 122
 QY 115 CYTAGTSCLSGWSSTSPQLRPLPTLRCANITTEHOKCENAYPGNTIDFWCASVOEG 174
 DB 123 EPRVGTCLVSGSSTSPQSLPSEWEFPDQLQCVNIHLSENKIRAYEKYVDIMLAGELEGG 182
 QY 175 GDSGSGPLVNCOSLQGIISWGODPCATTRKPGVYTKVCKYVDIMQETMKN 230
 DB 183 GDTCKGDSGGLCDGLVGLTISWGVPCGPBNKPGYTKLFTSWIKEMKKN 238
 RESULT 11
 Q63274 PRELIMINARY; PRT; 235 AA.
 AC Q63274;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Kallikrein (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
 RA Zintz C.B., Ma J.-X., Chao J., Chao L.;
 RT "Isolation and characterization of a new rat kallikrein cDNA with
 RT predominant expression in the kidney."
 RL Submitted (JAN-1995) to the EMBL/Genbank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR EMBL: U3839; AA58781.1; -;
 DR HSSP: P00759; 1TON.
 DR MEROPS: S01.410; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.

DR SMART: SM00020; TRYP_SPE; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease.
 FT NON_TER 1
 SQ SEQUENCE 235 AA; 26226 MW; 26160E9D3F7DC555 CRC64;

Query Match 46.5%; Score 587.5; DB 11; Length 235;
 Best Local Similarity 45.3%; Pred. No. 2.4e-53;
 Matches 107; Conservative 40; Mismatches 80; Indels 9; Gaps 2;

QY 2 IIRGFECKPHSOPWQALFEKTRLLCGATLIAPRWLTAAHCLKPRIVHIGOHNLQKE 61
 1 IIVGGYCKEKNQPMQWAVI--NRVLCGGVLIDPSWVITAAHCHYHYVHLLGRHNLFEDE 58
 DB 1 IIVGGYCKEKNQPMQWAVI--NRVLCGGVLIDPSWVITAAHCHYHYVHLLGRHNLFEDE 58
 QY 62 GCEOTRATESFPHPGFENSLPKN-----DHRNDIMLVKMASPVSTITNAVRPLTSSR 114
 DB 59 PFAQIRYVSQSPFHPDPNPFILMRHHTROTGYDSNDMLLHLSBPADITDGVKVIDLPT 118
 QY 115 CVTAGTSCILSGWGTSSTSPQLRPLPRLCANITIIHOKCENAVPGNITDTWCASVOEG 174
 DB 119 EPKVGSTCLVSGWGTSSTSPQLRPLSELDPDLCVNDILSNKCEATFRKVTDLMLCAGKLEG 178
 QY 175 GKDSQCGDSGGLVNCOSLOGIISWGDPACATRRKPGVYTRKCYVDIMQETMKN 230
 DB 179 GKDACNGDSGGLICDGLVGLTSMGVSVPCEPHNPGIYTRKIRKTSWIKEMKEN 234

RESULT 12
 Q9JUM70 PRELIMINARY; PRT; 261 AA.

AC 09JUM70;
 DT 01-OCT-2000 (TREMUREL. 15, Created)
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
 DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)
 DE Glandular kallikrein 21 (Similar to kallikrein 21).
 GN KIK21 OR GK21.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20534760; PubMed-11082197;
 RA Matsui H., Moriyama A., Takahashi T.;
 RT "Cloning and characterization of mouse Kik27, a novel tissue
 kallikrein expressed in testicular Leydig cells and exhibiting
 RT chymotrypsin-like specificity."
 RL Eur. J. Biochem. 267:6858-6865(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SALIVARY GLAND;
 RA Strausberg R.;
 RL Submitted (M06-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC EMBL: AB039276; BAA92319.1; -;
 CC EMBL: BC012243; AAL12243.1; -;
 DR HSSP; P00757; 1SGF.
 DR MEROPS; S01.038; -;
 DR MGD; MGI:892022; KIK21.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00089; trypsin.1
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease.
 SQ SEQUENCE 261 AA; 28690 MW; 608B976BC78E03BE CRC64;

Query Match 46.4%; Score 586.5; DB 11; Length 261;
 Best Local Similarity 43.9%; Pred. No. 3.4e-53;
 Matches 104; Conservative 45; Mismatches 81; Indels 7; Gaps 1;

QY 1 IIRGFECKPHSOPWQALFEKTRLLCGATLIAPRWLTAAHCLKPRIVHIGOHNLQKE 60
 DB 24 RIVGFCNEKNQSPWQWAVFPRNYKICGGVLINPWWVLTAAHCGNQYVNLGKRLFOH 83
 QY 61 EGCEOTRATESFPHPGFENSLPKN-----PKNRNDIMLVKMASPVSTITNAVRPLTSS 113
 DB 84 ESSAQHRLVSKSPFHPDPNPFILMRHHTROTGYDSNDMLLHLSBPADITDGVKVIDLPT 143
 QY 114 RCVTAGTSCILSGWGTSSTSPQLRPLPRLCANITIIHOKCENAVPGNITDTWCASVOE 173
 DB 144 EEPKVGSTCLVSGWGTSSTSPQLRPLSELDPDLCVNDILSNKCEATFRKVTDLMLCAGKLEG 203
 QY 174 GKDSQCGDSGGLVNCOSLOGIISWGDPACATRRKPGVYTRKCYVDIMQETMKN 230
 DB 204 GKDPICAGDSGGLICDGLVGLTSMGVSVPCEPHNPGIYTRKIRKTSWIKEMKEN 260

RESULT 13
 Q9N1Q1 PRELIMINARY; PRT; 261 AA.

AC 09N1Q1;
 DT 01-OCT-2000 (TREMUREL. 15, Created)
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
 DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)
 DE Tissue kallikrein.
 OS Saginus oedipus (Cotton-top tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Sagininae.
 OX NCBI_TaxId=9490;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21094033; PubMed-11177570;
 RA Olsson A.V.M., Persson A.M., Valtonen-Andre C., Lundvall A.;
 RT "Glandular kallikreins of the cotton-top tamarin: molecular cloning of
 the gene encoding the tissue kallikrein."
 RL DNA Cell Biol. 19:721-727(2000).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 CC EMBL: AF173845; AAF29490.1; -;
 CC HSSP; P00752; 2PKA.
 DR MEROPS; S01.160; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00089; trypsin.1
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPE; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease.
 SQ SEQUENCE 261 AA; 28815 MW; 7929E5C2AFB80E81 CRC64;

Query Match 45.9%; Score 579.5; DB 6; Length 261;
 Best Local Similarity 43.0%; Pred. No. 1.8e-57;
 Matches 102; Conservative 50; Mismatches 78; Indels 7; Gaps 1;

QY 1 IIRGFECKPHSOPWQALFEKTRLLCGATLIAPRWLTAAHCLKPRIVHIGOHNLQKE 60
 DB 24 RIVGFCNEKNQSPWQWAVFPRNYKICGGVLINPWWVLTAAHCGNQYVNLGKRLFOH 83
 QY 61 EGCEOTRATESFPHPGFENSLPKN-----LPKNRNDIMLVKMASPVSTITNAVRPLTSS 113
 DB 84 EDTAQFVFSKSPFHPDPNPFILMRHHTROTGYDSNDMLLHLSBPADITDGVKVIDLPT 143
 QY 114 RCVTAGTSCILSGWGTSSTSPQLRPLPRLCANITIIHOKCENAVPGNITDTWCASVOE 173
 DB 144 EGIEVGSTCLVSGWGTSSTSPQLRPLSELDPDLCVNDILSNKCEATFRKVTDLMLCAGKLEG 203
 QY 174 GKDSQCGDSGGLVNCOSLOGIISWGDPACATRRKPGVYTRKCYVDIMQETMKN 230

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OM protein - protein search, using sw model

Run on: December 23, 2002, 14:16:02 ; Search time 50 Seconds

(without alignments)
442,218 Million cell updates/sec

Title: US-09-856-320A-2_COPY_53_282

Perfect score: 1263
Sequence: 1 RIIRKFECKPHSQPMQALF.....GYTKVKCYIDWIOETMKN 230Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	686	54.3	260	2	neutropsin - mouse
2	610.5	48.3	265	2	KORP
3	605.5	47.9	261	2	trypsin (EC 3.4.21)
4	600.5	47.5	261	1	NGMSG
5	596.5	47.2	263	2	trypsin (EC 3.4.21)
6	596	47.2	248	2	trypsin (EC 3.4.21)
7	593	47.0	246	1	trypsin (EC 3.4.21)
8	590.5	46.8	261	2	trypsin (EC 3.4.21)
9	590	46.7	238	2	trypsin (EC 3.4.21)
10	589	46.6	246	1	trypsin (EC 3.4.21)
11	586.5	46.4	259	2	trypsin (EC 3.4.21)
12	582.5	46.1	261	2	trypsin (EC 3.4.21)
13	582.5	46.1	261	2	trypsin (EC 3.4.21)
14	579.5	45.9	261	2	trypsin (EC 3.4.21)
15	579	45.8	231	1	trypsin (EC 3.4.21)
16	578	45.8	232	1	trypsin (EC 3.4.21)
17	573	45.4	246	2	trypsin (EC 3.4.21)
18	572.5	45.3	259	1	trypsin (EC 3.4.21)
19	570.5	45.2	261	2	trypsin (EC 3.4.21)
20	570	45.1	247	1	trypsin (EC 3.4.21)
21	569.5	45.1	244	2	trypsin (EC 3.4.21)
22	569.5	45.1	261	1	trypsin (EC 3.4.21)
23	567	44.9	262	1	trypsin (EC 3.4.21)
24	566	44.8	229	1	trypsin (EC 3.4.21)
25	562	44.5	248	2	trypsin (EC 3.4.21)
26	561.5	44.5	257	2	trypsin (EC 3.4.21)
27	561.5	44.5	261	2	trypsin (EC 3.4.21)
28	558	44.2	243	2	trypsin (EC 3.4.21)
29	558	44.2	247	2	trypsin (EC 3.4.21)

30	556.5	44.1	261	1	semenogelase (EC 3
31	555	43.9	247	2	trypsin (EC 3.4.21)
32	554.5	43.9	231	2	trypsin (EC 3.4.21)
33	554.5	43.9	247	2	trypsin (EC 3.4.21)
34	553.5	43.8	259	2	trypsin (EC 3.4.21)
35	553.5	43.8	261	1	trypsin (EC 3.4.21)
36	553.5	43.8	261	2	trypsin (EC 3.4.21)
37	552	43.7	246	1	trypsin (EC 3.4.21)
38	552	43.7	256	1	trypsin (EC 3.4.21)
39	551.5	43.7	239	2	trypsin (EC 3.4.21)
40	548.5	43.4	261	2	trypsin (EC 3.4.21)
41	548	43.4	253	2	trypsin (EC 3.4.21)
42	547.5	43.3	261	1	trypsin (EC 3.4.21)
43	546.5	43.3	242	2	trypsin (EC 3.4.21)
44	546.5	43.3	242	2	trypsin (EC 3.4.21)
45	546.5	43.3	242	2	trypsin (EC 3.4.21)

ALIGNMENTS

RESULT 1
156559
neutropsin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: 156559
R:Chen, Z.L., Yoshida, S., Kato, K., Momota, Y., Suzuki, J., Tanaka, T., Ito, J., Nis
J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease
A:Reference number: 156559; M01D:95348817; PMID:7623137
A:Accession: 156559
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: GB:D30785; NID:g1648847; PIDN:BA06451.1; PID:g1020091
C:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRY>

Query Match 54.3% Score 686; DB 2; Length 260;
Best Local Similarity 52.8%; Pred. No. 1.9e-53;
Matches 121; Conservative 36; Mismatches 70; Indels 2; Gaps 2;

QY 1 RIIRKFECKPHSQPMQALFETRLCGATLIAPRWLTAAHCKLPRTYVHAGHNLQKE 60
Db 32 KILRGRECIPIHSPQMOALFQGERLIGCVLWGRWVLTAAHCKKQKVSRLGSHLSQSR 91
QY 61 EGCQTRATSEFHPGNNSLPKDRNDIMLYKASPVSTIYAVRPLTSSRCVTAQT 120
Db 92 DQPEQIOVAQSIQHPCCYNNSNP-EDHSHDITMLIRLQNSANLGDVKVQOLANLCPKVQ 150
QY 121 SCLISGMSSTSPOLRLPHTLRCAINTITIEHCKENAVPGNITPMWCASVQEGKDSQ 180
Db 151 KCIISGMSITVSPQBNPNPNTLNCALFVKIYSONKCEKRAVPGITTEBMCAG-SSNGADTCQ 209
QY 181 GDSCGPIVCDMGLGITSWGSDDPCGKPEKPGVYTRKICVYTWIKKTYMDN 258
Db 210 GDSCGPIVCDMGLGITSWGSDDPCGKPEKPGVYTRKICVYTWIKKTYMDN 258

RESULT 2
KORP
tissue kallikrein (EC 3.4.21.35) precursor - rat
N:Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 16-Jun-2000
C:Accession: A00944; A41429; A25137; JX0073; A23863; A33359
R:Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A:Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence
A:Reference number: A00944; M01D:93117659; PMID:6961406
A:Accession: A00944
A:Molecule type: mRNA

RESULT 15

TRPSTR

trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)

N:Contains: trypsinogen

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A90641; A90368; A00947

R:Charles, M.; Rovery, M.; Guidoni, A.; Desnuelle, P.

Biochim. Biophys. Acta 69, 115-129, 1963

A:Title: Su le trypsine et la trypsine de porc.

A:Reference number: A90641

A:Accession: A90641

A:Molecule type: protein

A:Residues: 1-10 <CHA>

R:Hermanson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.

Biochemistry 12, 3146-3153, 1973

A:Title: Determination of the amino acid sequence of porcine trypsin by sequenator analy

A:Reference number: A90368; MUID:73258692; PMID:4738933

A:Accession: A90368

A:Molecule type: protein

A:Residues: 9-231 <HER>

A>Note: at position 20, Ile and Val occur alternatively

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase; zym

F:1-231/Product: trypsinogen #status experimental <ZYM>

F:9-231/Product: trypsin #status experimental <APT>

F:9-224/Product: trypsin homology <TRY>

F:15-145,33-49,117-218,124-191,156-170,181-205/Disulfide bonds: #status predicted

F:48,92,185/Active site: His, Asp, Ser #status predicted

F:60,62,70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 45.8%; Score 579; DB 1; Length 231;

Best Local Similarity 47.6%; Pred. No. 5.2e-44;

Matches 110; Conservative 36; Mismatches 77; Indels 8; Gaps 4;

QY 1 RIKGFECRPHSQWQALFEKRLLCATLIAPRWLITAAHCLKPRYIVHLGQHLOKE 60

Db 8 KIVGGYTCANASIPYOVSLNSGSH-FCGSGSLNSQWVSAAHCKRSIQVRLGEHNIDVL 66

QY 61 EGCEQTRATESFPPGPFN-NSLPKDHNDIMLYKMASPVITWAVRPLTSSRCYTAG 119

Db 67 EGNEDFTIAAKITTHPNFNGTLD---NDIMLIKSSPATLNSRVATVSLPRSCAAAG 121

QY 120 TSCILSGWSTSPQLRLPHTLRACANITIEHKECENAYPGNITPDVWCASVOEGGKDC 179

Db 122 TBCILSGWGNTRKSSGSSIFSLQCLAKAPVLSDSCKSSYPGQITGNMTCVGFLEGKDC 181

QY 180 QGDSGGPLVNCQSLQGISWQDPCATIRKPGVYTKCKYVDWIOETMKN 230

Db 182 QGDSGGPVVNCQSLQGISWQYG-CAQKNKPGVYTKVCNVYMWIQGTIAN 231

Search completed: December 23, 2002, 14:22:43
Job time : 51 secs

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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/083554


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: PRIOR APPLICATION NUMBER: 60/085573
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085704
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/085697

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Alignment Scores:
Pred. No.: 1,18e-61
Score: 683.00
Percent Similarity: 70.67%
Best Local Similarity: 51.56%
Query Match: 54.08%
DB: 9
Gaps: 2

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US-09-856-320a-2_COPY_53_282 (1-230) x US-09-978-295a-394 (1-999)

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QY 21 GlulysThrArgleuleucysglYAlaThrleulealaproAgtTprleuleThra 40
Db 319 CAGGCGCAGCACTACTCTGTGGGGGTCTCTGTAGGTGGCAACTGGCTTACAGCT 378
QY 41 AlaHisCysleuysProArgTyrIleValHisleuGlyGlnHisAsnleuGlnLysGlu 60
Db 379 GCCACGTGTAATAAACCAATATACACAGTACGCTGGAGACACACAGCTTACAGATRAA 438

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QY 61 GlulGlyCysgluGlnThrAlaThrleuSerPheProHisProGlyPheAsnAsn 80
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QY 81 SerleuProAsnLysAspHisArgAsnAspIleMetleuValIlyMetAlaSerProAl 100
Db 499 AGC---GATGTGGAGGACACACCATATCTGATCTTTCACACTCGTGCAGCAGCA 555
QY 101 SerIleThrTrpAlaValArgProleuThrleuSerSerArgCysValThrAlaGlyThr 120
Db 556 TCCTCGGGGTCCAAAGTAAGCCATCAGCTCGCAGATCAATGACACCCAGCTGCGCAG 615
QY 121 SerCysleuIleSerGlyTyrPglySerThrSerSerProGlnleuArgleuProHisThr 140
Db 616 AAGTCACCGCTCTCAGCGCTGGGGCAGCTGTACACCTCCCGCAGAAATTTCCGTACACT 675
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QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 180
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QY 221 AspTyrIleGlnGlu 225
Db 913 GACTGATCAGCAGAG 927

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RESULT 6

US-09-978-697-394

Sequence 394, Application US/09978697

Patent No. US20020169284A1

GENERAL INFORMATION:

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: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Bolstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paonli, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630P1C27
: CURRENT APPLICATION NUMBER: US/09/978,697
: CURRENT FILING DATE: 2001-10-16

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;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	1,18e-61	Length:	999
Score:	683.00	Matches:	116
Percent Similarity:	70.67%	Conservative:	43
Best Local Similarity:	51.56%	Mismatches:	64
Query Match:	54.08%	Indels:	2
DB:	9	Gaps:	2

US-09-856-320A-2_COPY_53_282 (1-230) x US-09-978-697-394 (1-999)

QY 1 Arg1lellelysglypneglucyslybprohisserglnprotpglnalaleuophe 20
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QY 21 GluystrltharyleuyleucysglYAlaThrleuilealaProargtTpleuThrAla 40
Db 319 CAGGGCCAGCACTACTCTGTGGCGGCTGCTTGTAGTGGCAACTGGCTCTTACAGCT 378
QY 41 AlaHisCysleuysProargtYrileValHisleuglylnHisAsnleuGlnLysGlu 60
Db 379 GCCCAGCTGTAAAAAAGCAATATACAGAGTACGCTGGGAGACACAGCCTTACAGATAAA 438
QY 61 GlulglysglgluGlnThrArgThrAlaThrGluSerPheproHisProGlyPheAsnAsn 80
Db 439 GATGGCCAGGCAAGAAATACCTGTGCTTCACATCCACACACCCCTGCTACACAGC 498
QY 81 SerleuProAsnlyAspHisArgAsnAspIleuMetleuValLysMetAlaSerProVal 100
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Db 556 TCCCTGGGCTCCAAAGTGAAGCCATCAGCTGCGACATTCATCCACCACCTGCGGCAG 615
QY 121 SerCysleuileserglYtrpGlySerThrSerSerProGlnleuAgluProHisThr 140
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QY 221 AsprtleleGlnlu 225
Db 913 GACTGATCAGAGAG 927

RESULT 7

US-09-978-192A-394
Sequence 394, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P19
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.: 1.18e-61 Length: 999
Score: 683.00 Matches: 116
Percent Similarity: 70.67% Conservative: 43
Best Local Similarity: 51.56% Mismatches: 64
Query Match: 54.08% Indels: 2
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_53_282 (1-230) x US-09-978-192A-394 (1-999)

QY 1 Argillelelyselgphneglucyslpsprohlssetglprrttrpcinalaaleupne 20

: OTHER INFORMATION: Nucleotide sequence encoding Tumor Antigen Derived
 : OTHER INFORMATION: Gene-14 (77DG-14) protein; nt 1344-1360 NCBI accession
 : OTHER INFORMATION: #AA343629
 DS-09-796-294-6

Alignment Scores:	
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	Gaps: 2

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QY	21	GlulysThrArgleuleucysglYalathrLeuilealaProArgtrpIeueuthrala	40
Db	669	CAGGGCCAGCAACTACTCTGTGGGGGTTGCTTGTAGTGGCAACATGGGTCTCTACAGT	728
QY	41	AlahisCysleuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuInsglu	60
Db	729	GCCACACTGTAAAAACCGAAATACAGATGAGCTGTGGAGACACAGCTTACAGATAAA	788
QY	61	GlulGlyCysgluInTrpArgThrAlathGluSerPheProHisProGlyIleAsn	80
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QY	141	LeuArgCysAlaAsnIleThrIleileGluHisGlnLysCysGlnAsnAlaTrpProGly	160
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QY	161	AsnIleThrAspThrMetValLysAlaSerValGlnGluGlyGlyLysAspSerGln	180
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QY	181	GlyAspSerGlyGlyProLeuValLysAsnGlnSerLeuGlnGlyIleIleSerTrpGly	200
Db	1143	GGCGATTCGTGGAGGCCCCCTGGTGTGTGATGTGGCACTCCAGGCACTACATCTCGGGGC	1207
QY	201	GlnAspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpVal	220
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GENERAL INFORMATION:			
APPLICANT: Rosen et al.			
TITLE OF INVENTION: 36 Human Secreted Proteins			
FILE REFERENCE: P2022P1			
CURRENT APPLICATION NUMBER: US/09/739,907			
CURRENT FILING DATE: 2000-12-20			

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? PRIOR FILING DATE: 1998-01-07
? PRIOR APPLICATION NUMBER: 60/070,655
? PRIOR FILING DATE: 1998-01-07
? NUMBER OF SEQ ID NOS: 196
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 52
? LENGTH: 1381
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-739-907-52

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Alignment Scores:	
Pred. No.:	5.34e-58
Score:	649.50
Percent Similarity:	68.10%
Best Local Similarity:	50.86%
Query Match:	51.43%
DB:	10
Length:	1381
Matches:	118
Conservative:	40
Mismatches:	67
Indels:	7
Gaps:	4

US-09-856-320A-2_COPY_53_282 (1-230) x US-09-739-907-52 (1-1381)

OY		1	ArgIleIleLysGlyPheGluCysLeuProHisSerGlnProTrpGlnAlaIle--Leu	19
Dd		324	CGCATCAATCAATGGATTCGCAGTCCGGATATACGCCAACCAGCGGTGGACGGCGCTGTGG	383
OY		20	PheGluIystrHrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThr	39
Dd		384	CTAAGGCCAACCAACGCTACTGTGGGGCGGTGTGGTGATCCACAGTGGCTGTACG	443
OY		40	AlaAlaHisCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLys	59
Dd		444	GCCCCCACTCCAGGAAGAAGTTTGAAGTCCGTCCGCCACTCTCCCTCCACA	503
OY		60	--GlutIugLysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyIle	78
Dd		504	GTTATTGAATGTGGGACGACAGATTTCCAGGGGGTCAAATCCATCCCACCCGCGGTAC	565
OY		79	AsnAsnSerLeuProAsnLysASPHisArgAsnAspIleMetLeuValLysMetalaser	98
Dd		564	TCC-----CACCCGTGGCCACTCCAACCTCATGCTCATCAACAACTGACACGA	611
OY		99	ProvalSerIleHrrTPAlaValaIargProLeuHrHeuSerArGysValaThla	118
Dd		612	AGAAITGCTGCCACTAAAGATGTAGACCCATCAAGCTTCCTCTCATTTGTCCCTGTCT	671
OY		119	GlyThrSerCysLeuIleSerGlyTyrPglySerThrSerSerProGlnLeuArgLeuPro	138
Dd		672	GGGCAAAAGTCTCTTGCTGTGGCTGGGGGACAAACAAAGACCCTCCAAAGGCACTTCCT	721
OY		139	HishrLeuArgCysAlaAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyr	158
Dd		732	AAGTCTCCCGAGTCTTGAATATATAGGCTGTAAATCAGAAAAGTCCGAGATCTTAC	791
OY		159	ProGlyAsnIleThrAspTrpMetValCysAlaSerValGlnGluGlyGlyLysASPser	178
Dd		792	CCGAGACAGATAGATGACACACCATTTCTGCGCGGT--GACAAAGCAGTAGAGACTCC	848
OY		179	CysGlnGlyaspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSer	198
Dd		849	TGCCAGGAGTATTCCTGGGGGCGCTGTGTGTGCATAATGCTCCCTGCAGGGACATCGTCTCC	908
OY		199	TrpIylGlnAspProCysAlaIleThrArgLysProGlyAlaTyrTrpLysValCysLys	218
Dd		909	TGGGGAACATTAACCTTTGTCCCGGGCCCAACAGACCGGGGTGTCTACGAACCTGTGCAG	968
OY		219	TyrValAspTrpIleGlnIuThrMetLysAsnAsn	230

1	PRIOR FILING DATE: 1998-05-28	1	PRIOR APPLICATION NUMBER: 60/089801
2	PRIOR APPLICATION NUMBER: 60/087607	2	PRIOR FILING DATE: 1998-06-18
3	PRIOR FILING DATE: 1998-06-02	3	PRIOR APPLICATION NUMBER: 60/089907
4	PRIOR APPLICATION NUMBER: 60/087609	4	PRIOR FILING DATE: 1998-06-18
5	PRIOR FILING DATE: 1998-06-02	5	PRIOR APPLICATION NUMBER: 60/089908
6	PRIOR APPLICATION NUMBER: 60/087759	6	PRIOR FILING DATE: 1998-06-18
7	PRIOR FILING DATE: 1998-06-02	7	PRIOR APPLICATION NUMBER: 60/089947
8	PRIOR APPLICATION NUMBER: 60/087827	8	PRIOR FILING DATE: 1998-06-19
9	PRIOR FILING DATE: 1998-06-03	9	PRIOR APPLICATION NUMBER: 60/089948
10	PRIOR APPLICATION NUMBER: 60/088021	10	PRIOR FILING DATE: 1998-06-19
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15	PRIOR FILING DATE: 1998-06-04	15	PRIOR APPLICATION NUMBER: 60/090252
16	PRIOR APPLICATION NUMBER: 60/088028	16	PRIOR FILING DATE: 1998-06-22
17	PRIOR FILING DATE: 1998-06-04	17	PRIOR APPLICATION NUMBER: 60/090254
18	PRIOR APPLICATION NUMBER: 60/088029	18	PRIOR FILING DATE: 1998-06-22
19	PRIOR FILING DATE: 1998-06-04	19	PRIOR APPLICATION NUMBER: 60/090349
20	PRIOR APPLICATION NUMBER: 60/088030	20	PRIOR FILING DATE: 1998-06-23
21	PRIOR FILING DATE: 1998-06-04	21	PRIOR APPLICATION NUMBER: 60/090355
22	PRIOR APPLICATION NUMBER: 60/088033	22	PRIOR FILING DATE: 1998-06-23
23	PRIOR FILING DATE: 1998-06-04	23	PRIOR APPLICATION NUMBER: 60/090429
24	PRIOR APPLICATION NUMBER: 60/088326	24	PRIOR FILING DATE: 1998-06-24
25	PRIOR FILING DATE: 1998-06-04	25	PRIOR APPLICATION NUMBER: 60/090431
26	PRIOR APPLICATION NUMBER: 60/088167	26	PRIOR FILING DATE: 1998-06-24
27	PRIOR FILING DATE: 1998-06-05	27	PRIOR APPLICATION NUMBER: 60/090435
28	PRIOR APPLICATION NUMBER: 60/088202	28	PRIOR FILING DATE: 1998-06-24
29	PRIOR FILING DATE: 1998-06-05	29	PRIOR APPLICATION NUMBER: 60/090444
30	PRIOR APPLICATION NUMBER: 60/088212	30	PRIOR FILING DATE: 1998-06-24
31	PRIOR FILING DATE: 1998-06-05	31	PRIOR APPLICATION NUMBER: 60/090445
32	PRIOR APPLICATION NUMBER: 60/088217	32	PRIOR FILING DATE: 1998-06-24
33	PRIOR FILING DATE: 1998-06-05	33	PRIOR APPLICATION NUMBER: 60/090472
34	PRIOR APPLICATION NUMBER: 60/088655	34	PRIOR FILING DATE: 1998-06-24
35	PRIOR FILING DATE: 1998-06-09	35	PRIOR APPLICATION NUMBER: 60/090535
36	PRIOR APPLICATION NUMBER: 60/088734	36	PRIOR FILING DATE: 1998-06-24
37	PRIOR FILING DATE: 1998-06-10	37	PRIOR APPLICATION NUMBER: 60/090540
38	PRIOR APPLICATION NUMBER: 60/088738	38	PRIOR FILING DATE: 1998-06-24
39	PRIOR FILING DATE: 1998-06-10	39	PRIOR APPLICATION NUMBER: 60/090542
40	PRIOR APPLICATION NUMBER: 60/088742	40	PRIOR FILING DATE: 1998-06-24
41	PRIOR FILING DATE: 1998-06-10	41	PRIOR APPLICATION NUMBER: 60/090557
42	PRIOR APPLICATION NUMBER: 60/088810	42	PRIOR FILING DATE: 1998-06-24
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44	PRIOR APPLICATION NUMBER: 60/088824	44	PRIOR FILING DATE: 1998-06-25
45	PRIOR FILING DATE: 1998-06-10	45	PRIOR APPLICATION NUMBER: 60/090678
46	PRIOR APPLICATION NUMBER: 60/088826	46	PRIOR FILING DATE: 1998-06-25
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48	PRIOR APPLICATION NUMBER: 60/088858	48	PRIOR FILING DATE: 1998-06-25
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50	PRIOR APPLICATION NUMBER: 60/088861	50	PRIOR FILING DATE: 1998-06-25
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52	PRIOR APPLICATION NUMBER: 60/088876	52	PRIOR FILING DATE: 1998-06-25
53	PRIOR FILING DATE: 1998-06-11	53	PRIOR APPLICATION NUMBER: 60/090696
54	PRIOR APPLICATION NUMBER: 60/089105	54	PRIOR FILING DATE: 1998-06-25
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56	PRIOR APPLICATION NUMBER: 60/089440	56	PRIOR FILING DATE: 1998-06-26
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58	PRIOR APPLICATION NUMBER: 60/089512	58	PRIOR FILING DATE: 1998-06-26
59	PRIOR FILING DATE: 1998-06-16	59	PRIOR APPLICATION NUMBER: 60/091360
60	PRIOR APPLICATION NUMBER: 60/089514	60	PRIOR FILING DATE: 1998-07-01
61	PRIOR FILING DATE: 1998-06-16	61	PRIOR APPLICATION NUMBER: 60/091478
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63	PRIOR FILING DATE: 1998-06-17	63	PRIOR APPLICATION NUMBER: 60/091544
64	PRIOR APPLICATION NUMBER: 60/089538	64	PRIOR FILING DATE: 1998-07-01
65	PRIOR FILING DATE: 1998-06-17	65	PRIOR APPLICATION NUMBER: 60/091519
66	PRIOR APPLICATION NUMBER: 60/089598	66	PRIOR FILING DATE: 1998-07-02
67	PRIOR FILING DATE: 1998-06-17	67	PRIOR APPLICATION NUMBER: 60/091626
68	PRIOR APPLICATION NUMBER: 60/089599	68	PRIOR FILING DATE: 1998-07-02
69	PRIOR FILING DATE: 1998-06-17		

;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	6.4e-58	Length:	1570
Score:	649.50	Matches:	118
Percent Similarity:	68.10%	Conservative:	40
Best Local Similarity:	50.86%	Mismatches:	67
Query Match:	51.43%	Indels:	7
DB:	9	Gaps:	4

US-09-856-320a-2_COPY_53_282 (1-230) x US-09-992-598-308 (1-1570)

QY 1 ArgileilelsglyPheglucyslserProhiserGlnProtrglnAlaala---Leu 19
DB 549 CGCATCATCATCATGATCGGACGCGCATATGCACACCCAGCCCTGGCCAGCCGCGTGTG 608
QY 20 PheglulysThrArgleuleucysglYalThrleulelealProArgrTgpleuleuthr 39
DB 609 CTAAAGCCCCAACCACTCTACTGCGGGCGGTGTGTGCATCCACAGTGGCTGCTCACG 668
QY 40 AlaalaHsCysleuLysProArgrTyrIlleValHsLeuGlYglNHsAsnleuLInys 59
DB 669 GCCGCCACTGCGAGAGAAAGTTTTCAGAGTCGCTCGGCCACTACTCCCTGTCACCA 728
QY 60 --GlugluclyCysgluGlnThrArgrThraIaThrgluserPheProHsProglYpHe 78
DB 729 GTTATGATCATCGGAGAGATGTTCCAGGGGGGTCAATCATGCCACCCCTGGCTAC 788
QY 79 AsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaser 98
DB 789 TCC-----CACCCCTGGCCACTCTAACGACCTCATGCTCATCAACTCAACACAGA 836
QY 99 ProValSerIleThrTrpAlaValAlaProleuThrLeuSerSerArgCysValThrAla 118
DB 837 AGATTCCTCCCACTAAAGATGTCAGACCATCAACAGTCTCTCATGTCTCTGCT 896
QY 119 GlyThrSerCysLeuIleSerGlyYrPglYserThrSerProglInLeuArgrLeuPro 138
DB 897 GGGACAAAGTCTGCTGTGCGTGGCGGGGAGAACCAAGACCCCAAGTGCATCTCCCT 956
QY 139 HsThrleuArgrCysAlaAsnIleThrIleIleGluHsGlnLysCysgluAsnAlaTyr 158
DB 957 AAGGTCCCTCAGTCTGTAATATATCAGCTGCTAACTCAGAAAGGTGCGAGATCTTAC 1016
QY 159 ProglAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSer 178
DB 1017 CCGAGACAGATAGATGACACATGTCTGCGCGCT---GACAAAGCAGGTAGAGACTCC 1073
QY 179 CysGlnGlyAspSerGlyGlyProleuValCysAsnGlnSerLeuGlnGlyIleIleSer 198
DB 1074 TGCCAGGGTGAATCTGGGGGGCGTGTGTCGATGCTCCGTCAGAGACTGCTGCC 1133
QY 199 TrpGlyGlnAspProCysAlaIleThrArgrLysProglYalTyrThLysValCysLys 218
DB 1134 TGGGAGAGTTCACCTTGTGCCCGGCCCAACAGACCGGGTGTCTACAGCAACCTGTCAAG 1193
QY 219 TyrValAspTrpIleGlnGluThrMetLysAsnAsn 230
DB 1194 TTCACCAAGTGAATTCAGAAACCATTCAGGCCAAC 1229

RESULT 13
US-09-989-293A-308
Sequence 308, Application us/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US/09/989, 293A
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05

Db 789 TCC-----CACCTGGCCACTTAACGACCTCATGCTCAACTGAACAGA 836
Qy 99 ProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAla 118
Db 837 AGAATGCTCCCACTAAAGATGTCAGACCCATCAACGCTCTCTCATGTGCTCTCT 896
Qy 119 GlyThrSerCysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuPro 138
Db 897 GGGACAAAGTCTGTGCTGTGGGGGACAAACAGACGCCCCCAAGTCACTTCCCT 956
Qy 139 HisThrLeuArgCysAlaAsnIleThrIleLeuHisGlnIlyscysGlyAsnAlaTyr 158
Db 957 AAGTCTCCAGCTCTGAATATACAGCGTGAATCAGAAAAGTGGAGATGCTTAC 1016
Qy 159 ProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSer 178
Db 1017 CCGAGACAGATAGATGACACCATGTCTGCGCCGCT---GACMAAGCAGATAGACATCC 1073
Qy 179 CysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSer 198
Db 1074 TGGCAGGCTGATCTGGGGGCGCTGTGCTGCAATGCTCTCAGGAGACTGCTGCC 1133
Qy 199 TrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLys 218
Db 1134 TGGGAGATTAACCTTGCTGCGCGGCCCAACAGACCGGGTGTCTACAGCAACCTGCAAG 1193
Qy 219 TyrValAspTrpIleGlnGlyThrMetLysAsn 230
Db 1194 TTCACCAAGTGTATCCAGAAACCATCCAGGCCAAC 1229

RESULT 14
US-09-989-722-308
Sequence 308, Application us/09989722
Patent No. US20020072067A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989, 722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532

RESULT 15
US-09-989-723-308
Sequence 308, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C62
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,723
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
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PRIOR APPLICATION NUMBER: 60/087609
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PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030

PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	6.4e-58	Length:	1570
Score:	649.50	Matches:	118
Percent Similarity:	68.108	Conservative:	40
Best Local Similarity:	50.868	Mismatches:	67
Query Match:	51.438	Indels:	7
DB:	10	Gaps:	4

US-09-856-320A-2_COPY_53_282 (1-230) x US-09-989-723-308 (1-1570)

QY 1 ArgIleIleIleYsgIlyPheGtIuCYsIlySPronISerGInProTPrGlnAlaAla----Leu 19
DB 549 CGGATCATCAATGCGATGCGATATGCAACCCAGCGCGGCGGCGGTG 608
QY 20 PheGluIyIThrArgIleuCYsGlyAlaIThrIleuIleAlaProArgTrpIleuThr 39
:::||||| ||||||||| |||::: |||:::|||||

DB 609 CTAAAGCCCAACCAAGCTCTACTGCGGGCGGTGTGTCGATCCACAGTGGCTCAGC 668
QY 40 AlaAlaHisCYsIleuYsProArgTyrIleValHisIleuGlyGlnHisAsnIleuGlnYs 59
DB 669 GCGGCCCACTGACAGAGAAGATTTCAGAGTCGCGTCCGCCACATCCCTGTCCACA 728
QY 60 ---GluGluIyCYsGluGlnIThrArgThrAlaThrCysIleuSerPheProHisProGlyPhe 78
DB 729 GTTATATCAATCTGGCGACGAGATGTTCCAGGGGTCAATTCACCCGCCCTGGCTAC 788
QY 79 AsnAsnSerIleuProAsnIyAspHisArgAsnAspIleuIleuValIySmetAlaSer 98
DB 789 TCC-----CACCTGGCCACTCTAAGCAGCTCAAGCTCAAGCTCAAGCTCAAGCAGA 836
QY 99 ProValSerIleIThrTrpAlaValArgProIleuThrIleuSerArgCYsValThrAla 118
DB 837 AGATATGCTCCCACTAAGATGTCAGACCCATCAAGCTCTCCTCTCATTTGCTCCTGCT 896
QY 119 GlyThrSerCYsIleuIleSerGlyTyrGlySerThrSerSerProGlnIleuArgLeuPro 138
DB 897 GGGACAAAGTCYTGGTGTGTGCTGGGACAAACCAAGAGCCCAAGTGCACCTTCCCT 956
QY 139 HisThrIleuArgCYsAlaAsnIleThrIleIleGluHisGlnIyCYsGluAsnAlaTyr 158
DB 957 AAGTCTCCAGTGTGCTGAATATCAGCGTCTAAGTCAGAAAGGTGCGAGATGCTTAC 1016
QY 159 ProGlyAsnIleIThrAspTrpMetValCYsAlaSerValGlnIyGlyIySAspSer 178
DB 1017 CCGAGACAGATATGATGACACCATGTTCTGCGCGGT---CACAAAGCAGGTACAGACTCC 1073
QY 179 CysGlnIyAspSerGlyIyProIleuValCYsAsnGlnSerIleuGlnIyIleIleSer 198
DB 1074 TGCAGGCGTATTCGTGGGGGCGCTGTGTCGAATGGCCCTCCAGGAGCTGTGTC 1133
QY 199 TrpGlyGlnAspProCYsAlaIleThrArgIyAspProGlyValIyThrIySValCYsIyS 218
DB 1134 TGGGAGATTAACCTTGTGTGCCCGGCCACACAGACCGGGGTCTTACAGAACTCTGCAG 1193
QY 219 TyrValAspTrpIleGlnIyThrMetIySAsnAsn 230
DB 1194 TTCACCAAGTGAATCCAGAAACCATCCAGGCCAAC 1229

Search completed: December 23, 2002, 16:05:37
Job time : 95 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2002, 14:20:02 ; Search time 302 Seconds

(without alignments)
1715.098 Million cell updates/sec

Title: US-09-856-320a-2_COPY_53_282

Perfect score: 1263
Sequence: 1 RIITGFECKPHSQPMQALF.....GYTTKCKYVDWIEETWKN 230

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq.101002 -ORWT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdl
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09856320.8CGN.1.1.281.runat.23122002.113711.22684 -ICPU=6 -ICPU=3
-NO.XLPHY -NO.MMAP -LARGEOURRY -NEG.SCORES=0 -MAIT -LONGLOG -DEV.TIMEOUT=120
-MARN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1263	100.0	1106	AA222638	CASB12 nucleotide
2	1263	100.0	1158	AA222639	CASB12 derived fro
3	1263	100.0	1186	ABK92131	Prostate cancer-as
4	1263	100.0	1192	AA214842	Human P5133 gene c
5	1263	100.0	1204	AAA37072	Human PRO1279 (UNQ
6	1263	100.0	1204	AA521496	Human cDNA sequenc
7	1263	100.0	1204	AA543320	DNA encoding prote
8	1263	100.0	1204	AB195664	Human angiogenesis
9	1263	100.0	1204	AB188175	Human PRO1279 cDNA
10	1263	100.0	1292	ABK33732	Human secreted huma
11	1263	100.0	1301	AA561763	CDNA encoding huma
12	1263	100.0	1314	AA230222	CDNA encoding a hu
13	1263	99.2	1146	AAV84589	Human secreted pro
14	1253	99.2	1146	ABA83430	Human secreted pro
15	1253	99.2	1146	AAV84589	Human secreted pro
16	1251	99.0	1166	AAV14841	CDNA encoding huma
17	1240.5	98.2	934	AA561765	CDNA encoding huma
18	1233	97.6	1191	AA597777	Extended human sec
19	1232.5	97.6	1335	AA245672	Nucleotide sequenc
20	1221.5	96.7	1052	AA287798	Activation constru
21	1221.5	96.7	1052	AA552370	Nucleotide sequenc
22	1218	96.4	833	AAV42925	DNA encoding a hum
23	1067	84.5	1323	AA561764	CDNA encoding mus
24	916.5	72.6	618	ABK30233	Human G-protein-co
25	834	66.0	762	AAH31050	Human colon cancer
26	834	66.0	762	AAH31050	Human colon cancer
27	739	58.5	1375	AA526876	Human cDNA encodin
28	737	58.4	1365	AA541087	CDNA encoding nove
29	719	56.9	924	AA541692	CDNA encoding nove
30	719	56.9	924	AA526948	Human cDNA encodin
31	719	56.9	924	ABK41855	CDNA encoding nove
32	686	54.3	1332	AA199534	Mouse ischaemic co
33	686	54.3	1333	AA199534	Human neuropsin-en
34	686	54.2	1333	AA563251	Human neuropsin ge
35	686	54.2	963	AA530570	Human protease, pr
36	684	54.2	963	ABK31774	DNA encoding novel
37	684	54.2	1278	ABK48347	CDNA encoding nove
38	683	54.1	809	AA587560	DNA encoding novel
39	683	54.1	868	AA244182	Human neuropsin cd
40	683	54.1	905	AA211029	Human serine prote
41	683	54.1	942	AA211030	Human serine prote
42	683	54.1	944	AAV84052	Nucleic acid encod
43	683	54.1	999	AA234225	Human PRO322 nucle
44	683	54.1	999	AA234225	Human PRO322 (UNQ2
45	683	54.1	999	AA521441	Human cDNA sequenc

ALIGNMENTS

RESULT 1
AA222638
ID AA22638 standard; cDNA; 1106 BP.

AA22638;

08-DEC-1999 (first entry)

CASB12 nucleotide sequence.

neuropsin; cancer; assay; inhibitor; serine protease; immunogenic;

ds.

Homo sapiens.

Key 14..862 location/Qualifiers
CDS /*tag= a

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/product= CASB12
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W09949055-A1.

30-SEP-1999.

17-MAR-1999; 99WO-EP01894.

20-MAR-1998; 98GB-0006095.

(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

Bruck CEM, Cassart J, Coche T, Vinals-Bassols C,

WPI; 1999-580450/49.

P-PSDB; AAY42439.

New human serine protease CASB12, for treatment, prevention and diagnosis of cancer and autoimmune diseases -

Claim 10; Page 47; 58pp; English.

This is the nucleotide sequence of the CASB12 gene. The nucleotide sequence of AA222638 shows homology with neuropilin and the encoded protein AA124233 is structurally related to other proteins of the serine protease family, having homology and/or structural similarity with neuropilin. It is expected that as well as similar structure, these proteins will also share similar biological functions and properties. The CASB12 polypeptides and polynucleotides can be used to develop methods for identifying agonists and antagonists/inhibitors of these molecules, and thereby treating conditions associated with CASB12 polypeptide imbalance. The invention also provides for diagnostic assays for detecting diseases associated with inappropriate CASB12 polypeptide activity or levels.

Since CASB12 is either specifically expressed or highly over-expressed in tumors compared to normal cells, the polypeptides and polynucleotides of the invention are believed to be important immunogens for specific prophylactic or therapeutic immunization against tumors. The polypeptides and polynucleotides can therefore be targeted by antigen specific immune reactions (which result in the destruction of the tumor cell) or they can be used to diagnose the occurrence of tumor cells.

SQ Sequence 1106 BP; 247 A; 348 C; 287 G; 224 T; 0 other;

Alignment Scores:

Pred. No.:	1 64e-105	Length:	1106
Score:	163.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best local similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-856-320A-2_COPY_53_282 (1-230) x AA222638 (1-1106)

QY	1	ArgllellellysglyPhegluLcysLysProHisserInProtrpglnAlaIalePhe	20
Db	170	AGGATCATCAAGGGGTTTCGATGCGAACCCCTCATCTCCAGCCCTTGCGACGCCCTGTTTC	2299
QY	21	GlulysThrArgleuleuLcysGlyAlaIleThrleuIleAlaProArgtrpIeuleuThrAla	40
Db	230	GAGAGAGAGCGGGCTACTCTGTGGGGCGACCTCATCGCCCGAGATGGCTCTGCAGCA	289
QY	41	AlaHisCysleuLysProArgTyrIleValHisleuLysIlnHisAsnleuGlnLysGlu	60
Db	290	GCCCACTGCGCTCAAGCCCGGTCATATGTTTACTGGGGGACGACCAACTCCGAAAGGAG	349
QY	61	GlulysCysgluInThrArgtrpThrAlaIleThrGluSerPheProHisProGlyPheAsn	80
Db	350	GAGGCGTGTGAGCAGACCCGGACAGCCACATGAGTCCTTCCCCACCCCGGCTTCAACAC	409
QY	81	SerleuProAsnLysAspHisAlaGlnAsnAspIleMetleuValLysMetAlaSerProVal	100
Db	410	AGCGTCCCAACAAAGACACACCGCAATGACATCATGTGTGTGAAGAGGATCGCCAGTC	469

OY	101	SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValIleTrpAlaGlyThr	120
Db	470	TTCATCACCCTGGCGCTGTGCACACCCTACCCCTCTCTCAGCCTGTGTACAGCTGGGGACC	529
OY	121	SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuAlaGluProHisThr	140
Db	530	AGCTGGCGTCATTTCGGGTGGGGAGACAGCGTCCAGGCCCCAGTTAGCGCTGGCTCAACC	589
OY	141	LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGly	160
Db	590	TTCGCATCGGCCAACATCACCATATTGAGCAGCAGAAAGTGTGAAAGCGCTACCCGGC	649
OY	161	AsnIleThrAspTrpMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGln	180
Db	650	AACATCACAGACACCATTGCTGTGTGCCAGCGCTGCAGGAAGGGGCAAGGACTCTCCAG	709
OY	181	GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly	200
Db	710	GGTGACTCCGGGGGCCCTGCTGCTGTATACACAGTCTTCAAGGCATTATCTCTGGGC	769
OY	201	GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpVal	220
Db	770	CAGGATCCGTTGGCATCACCCGAAACCTGGTGTCTTACAGAAAGTCTCAATAATATGTG	829
OY	221	AspTrpIleGlnGluThrMetLysAsnAsn	230
Db	830	GACTGTGATCCAGAGACGATGAACAACAT	859

RESULT 2

ID	AAZ22639	standard;	CDNA;	1158	BP

AC AAZ22639;

DT 08-DEC-1999 (first entry)

CASB12 derived from Expressed Sequence Tag sequences

KW neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;

XX

XX

FT	CDS	84..932
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/product= CASB12

PN W09949055-A1.

PD 30-SEP-1999.

PF 17-MAR-1999; 99WO-EP01894.

PR 20-MAR-1998; 98GB-0006095.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Bruck CEM, Cassart J, Coche T, Vinals-bassols C

DR WPI; 1999-580450/49

XX
XX
XX

PT diagnosis of cancer

PS Claim 26; Page 49; 58pp; English

This is the n

CC tumor-associated antigens. The nucleotide sequence of AAZ22638 shows
CC homology with neuropsin and the encoded protein AAY42439 is structurally

CC related to other proteins of the serine protease family, having homology
CC and/or structural similarity with neuropilin. It is expected that as well
CC as similar structure, these proteins will also share similar biological
CC functions and properties.
CC The CASB12 polypeptides and polynucleotides can be used to develop
CC methods for identifying agonists and antagonists/inhibitors of these
CC molecules, and thereby treating conditions associated with CASB12
CC polypeptide imbalance. The invention also provides for diagnostic assays
CC for detecting diseases associated with inappropriate CASB12 polypeptide
CC activity or levels.
CC Since CASB12 is either specifically expressed or highly over-expressed
CC in tumors compared to normal cells, the polypeptides and polynucleotides
CC of the invention are believed to be important immunogens for specific
CC prophylactic or therapeutic immunization against tumors. The
CC polypeptides and polynucleotides can therefore be targeted by antigen
CC specific immune reactions (which result in the destruction of the tumor
CC cell) or they can be used to diagnose the occurrence of tumor cells
XX

SQ Sequence 1158 BP; 274 A; 359 C; 306 G; 219 T; 0 other;

Alignment Scores:

Pred. No.:	1,73e-105	Length:	1158
Score:	1263.00	Matches:	230
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-856-320A-2_COPY_53_282 (1-230) x AA222639 (1-1158)

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DB 240 AGGATCATCAAGCGGTGAGTGCACAGCCCTCCAGCCCTGGCAGCGCCCTGTC 299
QY 21 GluIySThrArgLeuLeuCysGlyAlaThrIleAlaProArgTrpLeuThrAla 40
DB 300 GAGAAAGCGCGCTACTCTGTGGGCGAGCTCAATCGCCCAATGAGTCTCTACAGCA 359
QY 41 AlaHisCysLeuIySProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLySglu 60
DB 360 GCCCATGCTCCATCAAGCCCGCTACATGATTCACCTGGGCGAGCAACCTCCACAAAGAG 419
QY 61 GluIySgIySgIyGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 80
DB 420 GAGGGCTGTAGAGCAGCCCGAGCAGCCAGTCTTCCGCCCGGCTTCAACAAAC 479
QY 81 SerLeuProAsnIySAspHisArgAsnAspIleMetLeuValIySMetAlaSerProVal 100
DB 480 AGCTCCCAACAAAGACACCGCATGACATCATGCTGTGAGATGGCATCGCCAGTC 539
QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
DB 540 TCCATTCACCTGGGCTGTGCGACCCCTCACCCCTCCACAGCTGTGACACTGGGACCC 599
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
DB 600 AGCTGCTCATTTCCGCTGGGCGAGCAGCTCCAGCCCAAGTTACCCCTGCTCACACC 659
QY 141 LeuArgCysAlaAsnIleThrIleIleGluHisGlnCysGluAsnAlaIyProGly 160
DB 660 TTGGATGCGCCCAACATCATCATATGAGCACAGAAAGTGTGAACGGCTACCCGGC 719
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlyGlyIySAspSerCysGln 180
DB 720 AACATCAGACAGACCATGTGTGTGCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 779
QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
DB 780 GGTGACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 839
QY 201 GlnAspProCysAlaIleThrArgLySProGlyValIyThrIySValIySlySlyVal 220
DB 840 CAGGATCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 899

QY 221 AspTrpIleGlnIyThrMetIySAsnAsn 230
DB 900 GACTGATCCAGAGACGATGACAGACAAAT 929

RESULT 3

ID ABR92131 standard; DNA: 1186 BP.

XX ABR92131;

DT 15-AUG-2002 (first entry)

XX Prostate cancer-associated DNA sequence #17.

XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

KW gene therapy; gene; ds.

XX Mammalia.

XX WO200230268-A2.

XX 18-APR-2002.*

XX 12-OCT-2001; 2001WO-US32045.

XX 13-OCT-2000; 2000US-0687576.

XX 08-DEC-2000; 2000US-0733288.

XX 08-DEC-2000; 2000US-0733742.

XX 24-JAN-2001; 2001US-263957P.

XX 16-MAR-2001; 2001US-276791P.

XX 06-APR-2001; 2001US-281922P.

XX 24-APR-2001; 2001US-286214P.

XX 30-APR-2001; 2001US-0847046.

XX 04-MAY-2001; 2001US-286589P.

XX (BOSB-) BOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Willson KE, Afar D, Hevezl P;

XX WPI; 2002-471335/50.

XX P-PSDB; ABG61816.

XX Detecting a prostate cancer-associated transcript in a cell in a

XX patient, useful for diagnosing prostate cancer (PC) or screening

XX modulators of PC, by determining if prostate cancer-associated genes

XX are expressed in a prostate tissue

XX Claim 22; Page 313; 436pp; English.

XX The present invention relates to methods of detecting a prostate

XX cancer-associated transcript in a cell from a patient. The method

XX comprises contacting a biological sample from the patient with

XX prostate cancer-associated polynucleotides (designated PC genes) that

XX selectively hybridize to a sequence that is at least 80% identical

XX to them. The prostate cancer-associated polynucleotide sequences

XX are differentially expressed in prostate tumour tissue or in

XX prostate cancer and are derived from the tissues of various

XX organisms such as humans or other mammals (e.g. mice, sheep and dogs).

XX The methods of the invention are useful for diagnosing and treating

XX prostate cancer in mammals. The prostate cancer-associated genes are

XX useful for diagnosing or treating prostate cancer, as well as for

XX identifying modulators of prostate cancer or agents that inhibit

XX prostate cancer. The nucleic acid sequences are particularly useful

XX in gene therapy, as a vaccine or in antisense applications.

XX ABR92115-ABR92263 represent prostate cancer-associated polynucleotide

XX sequences.

SQ Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;

Alignment Scores:

Pred. No.:	1.79e-105	Length:	1186
------------	-----------	---------	------

Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x ABR2131 (1-1186)

```

QY 1 ArgIleIleIleGlyPheGlyCysIleProHISerGlnProTrpGlnAlaIlePhe 20
   |||||
DB 182 AGGATCATCAAGGGGTTCAGTGCAGACCTCCTCCAGCCCTGGAGAGGAGCCGTTC 241
QY 21 GluIysThrArgLeuLeuGlyAlaIleHISLeuIleAlaProArgTrpLeuThrAla 40
   |||||
DB 242 GAGAACACGGGCTACTCTGTGGGGGAGCCCTATCGCCCCCAGATGGCTCCGACAGCA 301
QY 41 AlaHIScysLeuIysProArgTrpIleValHISLeuGlyGlnHISAsnLeuGlnIysGlu 60
   |||||
DB 302 GCCCACTGCTCAAGCCCGCTACATAGTTCACCTGGGAGCACAACCTCCAGAAAGAG 361
QY 61 GluGlyCysGlnGlnThrArgTrpAlaIleHISLeuSerPheProHISProGlyPheAsnAsn 80
   |||||
DB 362 GAGGGCTGTAGACAGACCCGAGACGACGACTCCTCCCGCAGCCCGGCTTCAACAC 421
QY 81 SerLeuProAsnIysAspHISArgAsnAspIleMetLeuValIysMetAlaSerProVal 100
   |||||
DB 422 AGCTTCCCCCAAGAACCCACCGCAATGACATCATGCTGTTGAAGTGGCATCGCCAGTC 481
QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValIleThrAlaGlyThr 120
   |||||
DB 482 TCCATCACCTGGGCTGTGGACCCCTCACCCTCTCTCCACGCTGTGTCACTGCTGGCACC 541
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHISThr 140
   |||||
DB 542 AGCTGCTCATTTCCGGCTGGGAGCAGACGTCACGCCCCAGTTACGCTGCTGCACACC 601
QY 141 LeuArgCysAlaAsnIleHISLeuIleGlnHISGlnIysCysGlnAsnAlaIleTrpGly 160
   |||||
DB 602 TTCGATGCCCCCAACATCACCATCATTTGAGCACGAAAGTGTAGAACGGCTTACCCGGC 661
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnIysGlyIysAspSerCysGln 180
   |||||
DB 662 AACATCACACACACATCATGCTGTGCCAGCTGCAGAGAAAGGGGCAAGAGCTCTGCGAC 721
QY 181 GlyAspSerGlyIysProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGly 200
   |||||
DB 722 GGTGACTCCGGGGGCTCTGTGTGTGTAACAGTCTCTCAAGGCAATTATCTCTGGGGC 781
QY 201 GlnAspProCysAlaIleHISArgIysProGlyValIleThrIysValCysIysTrpVal 220
   |||||
DB 782 CAGGATCCGTTGTCGATCACCCGAAAGCCGTGGTGTCTACACGAAAGTCTGCAATATATGTG 841
QY 221 AspTrpIleGlnIleuThrMetIysAsnAsn 230
   |||||
DB 842 GACTGATCCAGAGACGATGAAGAACAAAT 871

```

RESULT 4
 AAD14842
 ID AAD14842 standard; DNA: 1192 BP.

AC AAD14842;
 XX 01-NOV-2001 (first entry)
 DE Human PS133 gene contig.
 XX Human, PS133; prostate disease; cancer; immunogen; gene therapy; EST;
 KW expressed sequence tag; cytostatic; ds.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 CDS 107..859

FT /tag= a
 FT /product= "Human PS133 protein"
 FT /transl_except= (pos:188..196, aa:Cys-Pro)
 FT /transl_except= (pos:224..232, aa:Phe-Lys)
 DB: 22 Gaps: 0

US6232456-B1.

15-MAY-2001.

06-OCT-1997; 97US-0944483.

06-OCT-1997; 97US-0944483.

(ABBO) ABBOTT LAB.

Cohen M, Colpitts TL, Friedman PY, Granados E, Klass MR;
 Russell JC, Stewart KD, Stroupe SD;

WPI, 2001-366357/38.

P-SDB; AAE08017.

New PS133 polynucleotides, useful for detecting, diagnosing, staging, monitoring, prognosing, preventing, treating or determining the predisposition of an individual to a prostate disease, e.g. cancer - Claim 1; Column 71-74; 93pp; English.

The patent discloses PS133 polynucleotides and polypeptides which are indicative of prostate disease. The patent also provides a method for detecting PS133 protein in a test sample. The polynucleotides of the invention are useful for detecting, diagnosing, staging, monitoring, prognosing, preventing, treating or determining the predisposition of an individual to prostate diseases such as cancer. PS133-derived polynucleotides are used for the detection of normal or altered gene expression, in assays for detecting, amplifying or quantifying genes or nucleic acids relating to prostate tissue diseases and conditions, and to produce probes which can be used in the detection of nucleic acids in a sample. PS133 proteins are used as immunogens for the production of antibodies. PS133 sequences are also used in gene therapy. The present sequence is human PS133 gene contig.

Sequence 1192 BP; 279 A; 385 C; 290 G; 238 T; 0 other;

Alignment Scores:

Pred. No.: 1,8e-105 Length: 1192
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x AAD14842 (1-1192)

```

QY 1 ArgIleIleIleGlyPheGlyCysIleProHISerGlnProTrpGlnAlaIlePhe 20
   |||||
DB 167 AGGATCATCAAGGGGTTCAGTGCAGACCTCCTCCAGCCCTGGAGAGGAGCCGTTC 226
QY 21 GluIysThrArgLeuLeuGlyAlaIleHISLeuIleAlaProArgTrpLeuThrAla 40
   |||||
DB 227 GAGAACACGGGCTACTCTGTGGGGGAGCCCTATCGCCCCCAGATGGCTCCGACAGCA 286
QY 41 AlaHIScysLeuIysProArgTrpIleValHISLeuGlyGlnHISAsnLeuGlnIysGlu 60
   |||||
DB 287 GCCCACTGCTCAAGCCCGCTACATAGTTCACCTGGGAGCACAACCTCCAGAAAGAG 346
QY 61 GluGlyCysGlnGlnThrArgTrpAlaIleHISLeuSerPheProHISProGlyPheAsnAsn 80
   |||||
DB 347 GAGGGCTGTAGACAGACCCGAGACGACGACTCCTTCCCGCAGCCCGGCTTCAACAC 406
QY 81 SerLeuProAsnIysAspHISArgAsnAspIleMetLeuValIysMetAlaSerProVal 100
   |||||
DB 407 AGCTTCCCCCAAGAACCCACCGCAATGACATCATGCTGTTGAAGTGGCATCGCCAGTC 466

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PR 29-OCT-1998; 98US-0108500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106502.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 18-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
XX (GETH ) GENENTECH INC.
XX
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
PI WPI, 2000-237871/20.
XX P-PSDB; AAY99390.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/Ligand interactions
XX
XX Claim 2; Fig 101; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/Ligand interactions. The polypeptides and nucleotide sequences
CC encoding them have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention.
XX
XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
SQ

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Alignment Scores:
Pred. No.: 1,82e-105 Length: 1204
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

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US-09-856-320A-2_COPY_53_282 (1-230) x AAA37072 (1-1204)
QY 1 ArgIleIleIleSgIlypHeGlyucLySProHISserGlnProTrpGlnAlaIleuPhe 20
DB 166 AGGATCATCAAGGCGTTCGAGTCGAAGCCCTCCAGCCCTGGAGGAGCCCGTTTC 225
QY 21 GluLySThrArgLeuLeuSgIlyAlaThrLeuIleAlaProArgTrpLeuLeuTrpAla 40
DB 226 GAAACAACCGCGCTACTCTGTGGGCGACGCTCATGCCGCCAGATGCTCCGACAGCA 285
QY 41 AlaHIScysLeuIleuSProArgTrpIleValIleHISLeuGlyGlnHISasnLeuGlnLysGlu 60
DB 286 GCCCATGCTCTCAAGCCCGCTCATATGTTACCTGGGCGACGACAACTCCGAAAGAG 345

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QY 61 GluGlyCysGlnGlnThrArgThrAlaThrGluSerPheProHISProGlyPheAsn 80
DB 346 GAGGCGTGTGAGCAGACCCGAGACAGCCATGAGTCTCCGCCACCCGGCTTCAACAAC 405
QY 81 SerLeuProAsnLysAspHISArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
DB 406 AGCCTCCCAACAAGACCCCAAGACATCATGTGTGTGAAGTGGCATGCGCAGTCC 465
QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
DB 466 TCCATCACTGGGCTGTGGCACCCTTCACCTCTCTCCACGCTGTGTCACTGGCACC 525
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHISThr 140
DB 526 AGCTGCTCATTTCCGGCTGGGCGAGCAGCTCCAGGCCCAAGTTAGCGCTTCACACC 585
QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHISGlnLysCysGlnAsnAlaIleTrpGly 160
DB 586 TTGCGATGCCCAACATCACCATCATTTGACACACAGAAAGTGAAGACGCTACCCCGGC 645
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
DB 646 AACATCAACACACATGATGTGTGCGCAGGCTCAGGAAGGGGCGAAGACTCTCCGAC 705
QY 181 GlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
DB 706 GGTGACTCCGGGGGCCCTGTGCTGTGAACACATCTCTTCAAGCATTAATCTCTGGGG 765
QY 201 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpVal 220
DB 766 GAGGATCCGCTGCTGATCACCCGAAAGCTGTCTACAGAAAGTGTGCAAAATATG 825
QY 221 AspTrpIleGlnGlnIleThrMetLysAsn 230
DB 826 GACTGATCCAGAGACGATGAAGAACAT 855
RESULT 6
AA321496
ID AA321496 standard; cDNA; 1204 BP.
XX
XX NC AA321496;
XX
XX DT 24-OCT-2001 (first entry)
XX
XX DE Human cDNA sequence encoding for PRO1279 polypeptide.
XX
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200140466-A2.
XX
XX PD 07-JUN-2001.
XX
XX PF 01-DEC-2000; 2000MO-US32678.
XX
XX 01-DEC-1999; 99MO-US28301.
XX 01-DEC-1999; 99MO-US28634.
XX 02-DEC-1999; 99MO-US28551.
XX 02-DEC-1999; 99MO-US28564.
XX 02-DEC-1999; 99MO-US28565.
XX 09-DEC-1999; 99US-0170262.
XX 16-DEC-1999; 99MO-US30095.
XX 20-DEC-1999; 99MO-US30911.
XX 20-DEC-1999; 99MO-US30999.
XX 30-DEC-1999; 99MO-US31243.
XX 06-JAN-2000; 2000MO-US00277.
XX 06-JAN-2000; 2000MO-US00376.
XX 11-FEB-2000; 2000MO-US03565.

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PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07332.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
 PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2001-408281/43.
 DR P-PSDB: AAU12424.
 XX
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical .
 PS
 PS Claim 3; Fig 505; 813pp; English.
 XX
 CC AA521244-AA521518 encode for novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 CC
 XX
 XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 1.82e-105 Length: 1204
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-856-320A-2_COPY_53_282 (1-230) x AA521496 (1-1204)
 QY 1 ArgilleleuysGlypneGluCysAlaProHisSerGlnProTPrGlnAlaAlaLeuPhe 20
 Db 166 AGATCATCAAGGGGTGAGTGCAGAGCTTCCAGCCCTGCGAGGAGCCCTGTTG 225
 QY 21 GlulysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTPrLeuLeuThrAla 40
 Db 226 GAGAAAGACGGCGCTACCTGTGGGGCGACGCTATCGCCCAAGATGGCTCTGACAGCA 285
 QY 41 AlahiscysleuysProArgTPrIleValHisleuGlyGlnHisAsnLeuGlnLysGlu 60

Db 286 GCCCACTGCCTCAGCCCCCGCTACATAGTCACTGGGGGAGACAACTCCAGAGAGAG 345
 QY 61 GluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsn 80
 Db 346 GAGGGCTGTGAGCAGACCCGGAGACCCAGCTAGTCTTCCCCCAGCCGGCTTCAACAC 405
 QY 81 SerleuProAsnLysAspHisAlaArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
 Db 406 AGCCTCCCAACAAAGACACACCGCATGACATCATCTGGTGAAGATGGATCCGCACTC 465
 QY 101 SerIleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
 Db 466 TCCATCACCCTGGGTGTGCGACCCCTCACCTCTCCACCTGTGTACAGCTGGGACC 525
 QY 121 SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
 Db 526 AGCTGCTCATTTTCCGGTGTGGGGGAGCAGCTCCAGCCCGCATTCGCTTCACAC 585
 QY 141 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGly 160
 Db 586 TTGGGATGCGCCACATCACCATTCATTCAGACACAGAGTGTGAAGACGCTACCCGGC 645
 QY 161 AsnIleThrAspTrpMetValCysAlaSerValGlnGlyGlyLysAspSerCysGln 180
 Db 646 AACATCAGACAGACCATGTGTGTGCCAGCGTCAGAGAGGGGCGAAGACTCTGCCAG 705
 QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGly 200
 Db 706 GGTGACTCCGGGGGCCCTCTGCTGTACCAAGCTCTTCAAGGCAATATCTCTGGGGC 765
 QY 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
 Db 766 CAGATCGCTGTGGCATCACCAGGAGCTGTGTCTACAGAAAGTGTGAATATGTG 825
 QY 221 AspTrpIleGlnGlnIleThrMetLysAsnAsn 230
 Db 826 GACTGATCCAGGAGCATGATGAAGACAT 855
 RESULT 7
 ID AAF54320 standard; DNA: 1204 BP.
 XX
 AC AAF54320;
 DT 02-Apr-2001 (first entry)
 XX
 DE DNA encoding protein of the invention #51.
 XX
 KW Secreted; transmembrane; gene therapy; ss.
 OS Unidentified.
 XX
 PN WO200078961-A1.
 PD 28-DEC-2000.
 XX
 PD 18-FEB-2000; 2000WO-US04342.
 XX
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US30095.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI Watanabe CK, Williams PM, Wood WI;
XX WPI: 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO.
PT useful as hybridization probes, in chromosome and gene mapping and gene
therapy -
XX
PS Claim 2; Fig 101; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of
CC anti-sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents.
CC The nucleic acids may also be used in gene therapy.
XX
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:
Pred. No.: 1,82e-105 Length: 1204
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x AAF54320 (1-1204)

QY 1 ArgIleIleIleSGLYPheglucylsPProHISerGIInProTPrgInAlaAlaIleuPhe 20
Db 166 AGGATCATCAAGGGGTGAGTGCAGAGCCCTACCTCCAGCCCTGGAGGAGCCCTGTTC 225
QY 21 GluIlyThrArgLeuLeuGlyAlaIleuIleAlaIleuArgIleuLeuThrAla 40
Db 226 GAGAAAGCGGGCTACTGTGGGGAGCGCTCATGCCGCCAGATGGCTCTGACAGCA 285
QY 41 ALHIScysLeuLysPProATgTYrIleValHISleuGlyInHISAsnLeuGlnLysGlu 60
Db 286 GCCCAGCTGCTCAAGCCCGCTCATATGTTCACTGGGGAGAGCAACCTCCAGAGAG 345
QY 61 GluGlyCysGluGlnThrArgThrAlaIleuGluSerPheProHISProGlyIleAsnAsn 80
Db 346 GAGGCGTGTGAGCAGACCCGAGCAGCAGTCTCTCCACCCCGCTTCACACAC 405
QY 81 SerLeuProAsnLysAspHISArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
Db 406 AGCCTCCCAACAAAGACCAACCCCAATGACATATGCTGGTGAAGATGGATGCCAGTC 465
QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
Db 466 TCCATACACGGGGCTGTGGAGCCCTCACCCCTCTCTCAAGCGTGTGCACTGTGGAGC 525
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHISThr 140
Db 526 AGCTGCTCATTTCCGGCTGGGGGACACAGTCACAGCCCGCAGTTACGCTGCACAC 585
QY 141 LeuArgCysAlaAsnIleThrIleIleGluHISGlnLysGlnLysAsnAlaTYrProGly 160
Db 586 TTGCGATGGCGCCCAACATCATCATTTGAGCAGACAGAGTGTAGAAGCGCTTACCCGGC 645
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 180
Db 646 AACATACAGACACCATGTGTGTGTCAGAGCTCAGAGAGAGGGGCAAGGACTCTGCGAG 705
QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
Db 706 GGTGACTCGGGGGCGCTGTGTTGAACCAAGTCTCTCAAGCAGATTATCTCTGGGCG 765
QY 201 GlnAspProCysAlaIleThrArgLysProGlyValTYrThrLysValCysLysTYrVal 220

Db 766 CAGATCCGTTGCGAGTACACCCGAAAGCTGTGTACACGAAAGTCTGCAATATGTG 825
QY 221 AspTrpIleGlnGluThrMetLysAsnAsn 230
Db 826 GACTGATCCAGAGAGCAGATGAAGACAT 855

RESULT 8
ABL95664
ID ABL95664 standard; cDNA; 1204 BP.
XX
AC ABL95664;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related cDNA PRO1279 SEQ ID NO: 207.
XX
KW Human: angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiac; cytosolic; antiangiogenic; hypotensive; vulnery;
KW antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806889.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
PA (GENTECH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PAN/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W.
XX
DR WPI: 2002-171999/22.
DR P-PSDB; ABB95526.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 1; Fig 207; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention.
XX
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:
Pred. No.: 1,82e-105 Length: 1204
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x ABL95664 (1-1204)
QY 1 ArgIlellelysglypnehlucylsypProHisSerGlnProTrpGlnAlaIalaIeuphe 20
DB 166 AGGATCAATCAAGGGGTTGAGTGCAGACCTCACTCCAGCCCTGGCAGCCCTGTTTC 225
QY 21 GluIysThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40
DB 226 GAGAAAGACGGGCTACGTCTGTGGGGGAGCGCTCATCGCCCGCAAGATGGCTCGACAGCA 265
QY 41 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
DB 286 GCCACAGCTCTCAAGCCCTCATAGTTCACCTGGGAGACCAACCTCCAGAGAGAG 345
QY 61 GluGlyCysGluGlnThrArgTrpAlaThrGluSerPheProHisProGlyPheAsn 80
DB 346 GAGGGCTGTGAGCAGACCCGACAGCCACTGAGTCTCTCCCAACCCCGGCTTCAACAC 405
QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
DB 406 AGCGTCCCAACAAAGACCGACGATGATCATGTGTGTAAGATGGATGCCAGTC 465
QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
DB 466 TCCATCAACCTGGGCTGTGACCCCTCACCTCTCTCAAGCTGTGTCACTGCTGGCACC 525
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
DB 526 AGCTGCTCTATTTCGGCTGGGAGACGTCACAGCCGCCAGTTACGCTGCTCAACACC 585

QY 141 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaIaTrpGly 160
DB 586 TTGGGATGGCCCAACATCACCATCATTTGAGACCAAGAGTGAAGACGCTACCCGGC 645
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 180
DB 646 AACATTCACAGACACCAATGAGTGTGTCACCGTCAGAGAGGGGCAAGACTCTCCAC 705
QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
DB 706 GGTGACTCCGGGGGCCCTTGCTGTGTACCAAGTCTTCAAGCCATTATCTCTGGGGC 765
QY 201 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpVal 220
DB 766 CAGATCCGTTGGTGATCACCCGAAAGCCTGCTGTACAGAAAGTGTCAAAATATGTG 825
QY 221 AspTrpIleGlnGluThrMetLysAsnAsn 230
DB 826 GACTGGATCCAGAGACGATGAGAACAAAT 855

RESULT 9
ABL88175
ID ABL88175 standard; cDNA; 1204 BP.
XX
AC ABL88175;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO1279 cDNA sequence SEQ ID NO:207.
XX
KW Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial stenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PE 20-JUN-2001: 2001WO-US19692.
XX
PF 23-JUN-2000: 2000US-213637P.
XX
PR 20-JUL-2000: 2000US-219556P.
PR 25-JUL-2000: 2000US-220624P.
PR 25-JUL-2000: 2000US-220664P.
PR 28-JUL-2000: 2000WO-US20710.
PR 02-AUG-2000: 2000US-222695P.
PR 17-AUG-2000: 2000US-0643657.
PR 23-AUG-2000: 2000WO-US23522.
PR 24-AUG-2000: 2000WO-US23328.
PR 07-SEP-2000: 2000US-230978P.
PR 18-SEP-2000: 2000US-0664610.
PR 18-SEP-2000: 2000US-0663550.
PR 24-OCT-2000: 2000US-242922P.
PR 08-NOV-2000: 2000US-0709238.
PR 08-NOV-2000: 2000WO-US30952.
PR 10-NOV-2000: 2000WO-US30873.
PR 01-DEC-2000: 2000WO-US32678.
PR 20-DEC-2000: 2000US-0747259.
PR 20-DEC-2000: 2000WO-US34956.
PR 22-JAN-2001: 2001US-0767609.
PR 28-FEB-2001: 2001US-0796498.
PR 28-FEB-2001: 2001WO-US06520.
PR 01-MAR-2001: 2001WO-US06666.
PR 09-MAR-2001: 2001US-0802706.
PR 14-MAR-2001: 2001US-0808689.

PA (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2002-172001/22.
 DR P-PSDB; AAU83684.
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 XX Claim 2; Figure 185; 359pp; English.
 XX
 XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABR33536-ABR33657 represent human
 CC PRO protein coding sequences of the invention.
 XX
 XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 S0
 Alignment Scores:
 Pred. No.: 1,82e-105 Length: 1204
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-856-320A-2_COPY_53_282 (1-230) x ABR33628 (1-1204)
 QY 1 Argillelelysglypneglucylslysfrohisserglnprotrpglnalalauephe 20
 DB 166 AGGATCATCAAGGGGTGAGTGCAGAGCCCTCAGCCCTGGCAGGAGCCCTGTTC 225
 QY 21 Glnusthraraglleuucysglyalathrleullealaprohrgtprleuethala 40
 DB 226 GAGAAGACGGCGCTACTCTGTGGCGCGCTCATGCCCGCAGATGGCTCTGACAGCA 285
 QY 41 Alahtscylsleuysproargtyrillevalhtsleuglnhtsasnleuglnlysglu 60
 DB 286 GCCCACTGCTCAAGCCCGCTACATAGTCACTGGGGCGACACACTCCAGAGGAG 345
 QY 61 Glnuglycysgluglnthraragthralathrgluberphrohisprogllyphasnasn 80
 DB 346 GAGGCGCTGTGACAGACCCGAGACAGCCACTGAGTCCCTCCGCCACCCGGCTTCAACAC 405
 QY 81 Serleuproabnlyshasphialasnasprlleuethvallysmetalaserproval 100
 DB 406 AGCCTCCCAACAAAGACACCGCATGATCATGTGGTGAAGATGGATCGCCACTC 465
 QY 101 Serlethrtrpalaalavalargproleuthrleuseraseragcysvalthralaglythr 120
 DB 466 TCCATACACTGGCTGTGCGACCCCTCACCCTCTCTACAGCTGTGTACTGCTGGCACC 525
 QY 121 Sercysleulleiserglytyrpglyserthrserserproglinleuargleuprohisthr 140
 DB 526 AGCTGCCCATTTCCGGCTGGGCGAGCAGCTCCAGCCCGCATTAAGCCTCCACACACC 585
 QY 141 Leuargcysalaaanllethrilleleuglnhtslnlyscysgluasnaltatyrprogly 160

DB 586 TTGGCATCGCCACACATACATCATTTAGACACCAAGAGTGTGAAAGCGCTACCCCGGC 645
 QY 161 AsnillethrarraspthrmetvalcysalaserValGlnluglyglylyAspserCysgln 180
 DB 646 AACATCAGACAGACCATGTGTGTGCCAGCTGCAGGAAGGGCGGAGATCTCTGCCAG 705
 QY 181 GlyaspserglyglyProleuValCysasnGlnserleuglnGlylleIleSertprgly 200
 DB 706 GGTGACTCGGGGGGCCCTCTGTGTGTAACACAGTCTCTTCAAGCATTAATCTCGGGGC 765
 QY 201 GlnaspprocysAlaallethrArghysproglValIYrthllyValCyslystYrVal 220
 DB 766 CAGATCCGTGTGCATACCCGAAAGCTGTGTCTACAGGAAGTCTGCAAAATATGTG 825
 QY 221 AsprrpilleglnluThrMetlysasn 230
 DB 826 GACTGATCCAGAGACGATGAAACAT 855
 RESULT 11
 ID ABA83372 standard; cDNA; 1292 BP.
 XX
 AC ABA83372;
 XX
 DT 07-FEB-2002 (first entry)
 DE
 XX Human secreted protein gene 179 SEQ ID NO:189.
 KW Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 KW cytosolic; cardiant; vascular; anti-angiogenic; ophthalmological;
 KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;
 KW antiparkinsonian; antitubercial; gene therapy; vaccine; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KW Gaucher's disease; cardiovascular disease; Schmitz syndrome; chemotaxis;
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;
 KW Parkinson's disease; infectious disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162891-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 21-FEB-2001; 2001WO-US05614.
 XX
 XX 24-FEB-2000; 2000US-184836P.
 PR 29-MAR-2000; 2000US-193170P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI NI J, Edner R, Lafleur DM, Moore PA, Olsen HS, Rosen CA;
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CU, Ferrie AM, Fan P;
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
 PI Zeng Z, Greene JM;
 XX
 DR WPI: 2001-625724/72.
 DR P-PSDB; ABB50479.
 XX
 PT Nucleic acids encoding 207 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 XX Claim 1; Page 1032; 1533pp; English.
 PS
 XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.

CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimer's; vascular;
 CC antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. sclinitar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA8185 to
 CC ABA8193 and ABB50300 represent sequences used in the exemplification of
 CC the present invention.

XX
 XX Sequence 1292 BP; 319 A; 387 C; 329 G; 253 T; 4 other;

Alignment Scores:
 Pred. No.: 2e-105 Length: 1292
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x ABA83372 (1-1292)

QY 1 ArgIleIleIysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaIleLeuPhe 20
 Db 267 AGGATCTATCAAGGGGTTGAGTGCAGACCTCCTCCAGCCCTGGCAGGAGCCCTGTC 326
 QY 21 GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThAla 40
 Db 327 GAGAGAGCGGGCTACTCTGTGGGCGACGCTATGCCGCCAGATGGCTCTCAGACGCA 386
 QY 41 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
 Db 387 GCCCAGCGCTCAAGCCCCCTCATATGATTCACCTGGGCGACACCAACCTCCAGAAAGAG 446
 QY 61 GluGlyCysGlnGlnIlePheArgTrpAlaThrGlnSerPheProHisProGlyPheAsnAsn 80
 Db 447 GAGGGGCTGAGAGACCCGCGAGCCACTGAGCTCTCCCAACCCCGGCTTCAACACAC 506
 QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
 Db 507 AGCCTCCCAACAAGACCAACCGCAATGACATGCTGTGAAGAGCGATGCCACAGTC 566
 QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
 Db 567 TCCATCTACCTGGGCTGTGCGACCCCTCACCTCTCCACGCTGTGTGCACTGCTGGCACC 626
 QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
 Db 627 AGGTGCTCTATTCCTGGGCTGGGAGACGCTCCAGCCCAAGTACGCCCTGCTCACACC 686
 QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIleTrpGly 160
 Db 687 TTTCGATGCCCAACATCATCATTTGAGCACCAGAGGTGAGAAAGCCCTACCCGGG 746
 QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnLysLysAspSerCysGln 180
 Db 747 AACATCACAGACACCAATGGGTGTGCGACGGTCCAGAGAGGGGCAAGGACCTCTCGCAG 806
 QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnLysIleLeuSerTrpGly 200
 Db 807 GGTGACTCCGGGGGCTCTGTCTTAACCAATCTCTTCAAGGCAATTATCTCTGGGG 866
 QY 201 GlnAspProCysAlaIleThrArgLysProGlyValIleTrpThrLysValCysLysTrpVal 220
 Db 867 CAGGATCCGCTGCTGATCAACCCGAAAGCCCTGTGTCTACACGAAAGTCTGCAATATGTG 926

QY 221 AspTrpIleGlnGlnIleThrMetLysAsnAsn 230
 Db 927 GACTGATCCAGAGACGATGAGAAACAAT 956

RESULT 12
 ID AAA61763 standard; cDNA; 1301 BP.
 XX
 AC AAA61763;
 XX
 XX 23-OCT-2000 (first entry)
 DE
 DE cDNA encoding human serine protease BSSP6 (hBSSP6) SEQ ID NO.1.
 XX
 XX BSSP6; serine protease; human; hBSSP6; mouse; mBSSP6; brain;
 KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
 KW epilepsy; cancer; inflammation; infertility; pancreatitis;
 KW prostatic hypertrophy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200031257-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 19-NOV-1999; 99WO-JP06476.
 XX
 PR 20-NOV-1998; 98JP-0347802.
 XX
 PA (FUSO) FUSO PHARM IND LTD.
 XX
 PI Demura H, Okui A, Kominami K, Yamaguchi N, Mitsui S;
 XX
 DR WPI: 2000-40067/34.
 XX
 DR P-PsDB; AAB11712.
 XX
 PT Serine protease BSSP6, useful in detecting homologs, mutants and
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
 PT using blood or other tissues
 XX
 PS Claim 2; page 67-69; 94pp; Japanese.
 XX
 XX The invention relates to novel serine proteases designated BSSP6
 CC (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-A61765).
 CC The invention also relates to vectors and transformants comprising BSSP6
 CC nucleic acids; transgenic animals in which the expression level of BSSP6
 CC can be varied; and an mBSSP6 knockout mouse. The invention additionally
 CC encompasses anti-BSSP6 antibodies and methods of production of such
 CC antibodies, methods of BSSP6 detection using the antibodies, and the
 CC use of BSSP6 proteins or fragments as diagnostic markers for certain
 CC medical conditions. Nucleotides encoding BSSP6 were initially
 CC isolated in a human brain cDNA library using degenerate PCR primers
 CC (AA61795-A61796) based on conserved regions of serine proteases. The
 CC BSSP6 serine proteases and nucleotides encoding them are useful in
 CC detecting homologues, mutants and polymorphic variants in biological
 CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
 CC and spleen) as diagnostic markers for conditions such as Alzheimer's
 CC disease, epilepsy, cancer, inflammation, infertility and prostatic
 CC hypertrophy. Sequences AAA61763 and AAA61765 represent cDNAs encoding
 CC human BSSP6 variants (hBSSP6), and sequence AAA61764 represents cDNA
 CC encoding murine BSSP6 (mBSSP6).
 XX

SO Sequence 1301 BP; 332 A; 387 C; 330 G; 252 T; 0 other;

Alignment Scores:
 Pred. No.: 2.01e-105 Length: 1301
 Score: 1263.00 Matches: 230
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

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US-09-856-320a-2_COPY_53_282 (1-230) x AAA61763 (1-1301)
QY 1 Argillelelysglypneglucylslyprohisserglnprotrpglnalaaleuphe 20
Db 269 AGGATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGGCAGGAGCCCTGTC 328
QY 21 GlulysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40
Db 329 GAGAAAGAGCGCGTACTGCTGGGGCGACGCTCATCCGCCAGATGGCTCCTGCAGACA 388
QY 41 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
Db 389 GCCCACTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGAGACAACTCCAGAGAGAG 448
QY 61 GluGlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 80
Db 449 GAGGGCTGTGAGCAGACCCGGAGACCCACTGAGTCTTCCCCACCCCGGCTTCAACAG 508
QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
Db 509 AGCTTCCCAACAAAGACACCCGCAATGACATGCTGTGAGAGATGGCATCGCAGCTC 568
QY 101 SerLeuThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
Db 569 TCCATCACTGGGTGCTGCGACCCCTCACCTCTCTCACCTGTGCTGCTGGCAGCC 628
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
Db 629 AGCTGCCCATTTCCGGCTGGGGGAGACAGCTCCAGCCCGGATTAAGCTCTCCACAGCC 688
QY 141 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGly 160
Db 689 TTGGGATGCGCGCAACATCATCATGAGCAGCAGAAAGTGTGAGAAAGCGCTACCCGCGC 748
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
Db 749 AACATCAAGACACCATGCTGTGCGCAGCTGAGGAGGAGGAGAGAGACTCTGCGCAG 808
QY 181 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
Db 809 GGTGACTCGGGGGGCCCTGCTGTGTAACAGTCTCTCAAGCATTAATCTCTGGGGC 868
QY 201 GlnAspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTrpVal 220
Db 869 CAGGATCCGCTGCGATCAGCAGCCGGAAGCGTGTGTACAGCAAAAGCTGCAATATGCTG 928
QY 221 AspTrpIleGlnIuThrMetLysAsnAsn 230
Db 929 GACTGGATCCAGAGAGCATGAGAAACAT 958

RESULT 13
AAZ30222
ID AAZ30222 standard; cDNA; 1314 BP.
AC AAZ30222:
XX 11-FEB-2000 (first entry)
XX cDNA encoding a human prostate-associated serum protease (PRASP).
XX
KW Human; prostate-associated serum protease; PRASP; neuropsin; PSA;
KW Incyte clone 2723646; reproductive disorder; cancer;
KW abnormal prolactin production; infertility; tubal disease;
KW ovulatory defect; endometriosis; polycystic ovary syndrome;
KW autoimmune disorder; ectopic pregnancy; breast cancer;
KW abnormal spermatogenesis; testicular cancer; adenocarcinoma; leukaemia;
KW lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 128..976

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FT FT /*tag- a
FT FT /product= "prostate-associated serum protease"
FT FT 146..181
FT FT /*tag- b
FT FT /note= "these nucleotides are separately claimed
FT FT misc.feature
FT FT 344..382
FT FT /*tag- c
FT FT /note= "these nucleotides are separately claimed
FT FT misc.feature
FT FT 551..589
FT FT /*tag- d
FT FT /note= "these nucleotides are separately claimed
FT FT under claim 10"

PN W09941387-A2.
PD 19-AUG-1999.*
PX
PF 05-FEB-1999; 99WO-US02571.
PR 17-FEB-1998; 98US-0025059.
XX
PA (INCY- ) INCYTE PHARM INC.
PI Tang YT, Corley NC, Guegler KJ;
XX WPI: 2000-012993/01.
DR P-PSDB: AAY43636.
XX
PT New prostate-associated serum protease and polynucleotides which
PT identify and encode PRASP, useful for treating reproductive disorders
PT and cancer
XX
PS Claim 7; Fig 1A-D; 67pp; English.
XX
CC The present sequence encodes a human prostate-associated serum protease
CC (PRASP). The protein shows homology to neuropsin, a brain-specific
CC protease in mice, and PSA, a prostate-specific protease in humans.
CC Nucleic acids encoding PRASP were first identified in Incyte clone
CC 2723646 from the lung tumour cDNA library. Pharmaceutical compositions
CC containing PRASP, or antibodies to PRASP, and mimetics, agonists,
CC antagonists or inhibitors of PRASP, are used for treating or preventing
CC a reproductive disorder or cancer. Examples of reproductive disorder
CC include, abnormal prolactin production, infertility, tubal disease,
CC ovulatory defects, endometriosis, polycystic ovary syndrome, autoimmune
CC disorders, ectopic pregnancy, breast cancer, abnormal spermatogenesis
CC and testicular cancer. Examples of cancers which may be treated or
CC prevented include adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma,
CC sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder,
CC bone, bone marrow, brain, breast, cervix, penis, prostate, salivary
CC glands, skin, spleen, testis, thymus, thyroid and uterus. A vector
CC capable of expressing PRASP or an agonist which modulates the activity of
CC PRASP may be administered to treat or prevent a reproductive disorder or
CC cancer.
XX
SQ Sequence 1314 BP; 320 A; 400 C; 337 G; 257 T; 0 other:
XX
XX
Alignment Scores:
Pred. No.: 2.04e-105 Length: 1314
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x AAZ30222 (1-1314)
QY 1 Argillelelysglypneglucylslyprohisserglnprotrpglnalaaleuphe 20
Db 284 AGGATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGGCAGGAGCCCTGTC 343
QY 21 GlulysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40

```

|||||
Db 344 GAGAAAGCGGCGCTACTGTGGGGGAGCGCTATGCGCCCAAGATGCTCTGACAGCA 403
QY 41 AlahiscysleuylsProAqTYrIleValHisleuGIylnHisAsnleuGIylnGlu 60
Db 404 GCCCACTGCTCAAGCCCCCTACATAGTTCACCTGGGGAGCAACAATCCAGAGAG 463
QY 61 GluGIyCysGIuGIlnHrArqHrAlaThrGluSerPheProHisProGIyPheAsnAsn 80
Db 464 GAGGGCTGTAGAGAGACCCGAGCAGCCATGAGTCTTCCCCCAGCCCCGCTCAACAC 523
QY 81 SerleuProAsnIysAspHisArgAspAspIleMetleuValIysMetIAsaSerProVal 100
Db 524 AGCTCCCAACAAAGACCAACCGCATGACATGCTGTGTAAGATGAGCATGCCAGTC 583
QY 101 SerIleHrTPAlaValAlaGrProleuThrLeuSerSerArgCysValIThrAlaGIyThr 120
Db 584 TTCATACCTCGGGCTGTGGAGACCCCTACCCCTCTCCACAGCTGTGTACATGCTGGAC 643
QY 121 SerCysleuIleSerGIyTrpGIySerThrSerSerProGIlnleuArgleuProHisThr 140
Db 644 AGCTGCTCATTTCCGGCTGGGAGAGACCTCCAGCCCCAGTTAGCCTGCTGACACAC 703
QY 141 LeuArgCysAlaAsnIleThrIleleGIlnHisGIlnIysCysGIlnAsnAlaTYrProGIy 160
Db 704 TTCGATGCGCGCAACATCACATCATTTAGACACCAAGATGAGAACGCGCTACCCGGC 763
QY 161 AsnIleHrAspThrMetValCysAlaSerValGIlnGIuGIyGIyAspSerCysGIln 180
Db 764 AACATCACACACACATCATGTGTGTCCAGGCTGACAGAGAGGGGCAAGAGCTCTGCGAG 823
QY 181 GlyAspSerGIyGIyProleuValCysAsnGIlnSerleuGIlnGIyIleIleSerTrpGIy 200
Db 824 GTTGATCTCCCGGGGCGCTGTGTGTGAACCACTCTTCAAGGACATTAATCTCTGGGCG 883
QY 201 GluAspProCysAlaIleThrArgIysProGIyValTYrThrIysValCysIysTYrVal 220
Db 884 CAGGATTCGGTGTGATGACACCGAAGCTGTGTCTACGAAAGTGTCAATATATGTG 943
QY 221 AspTrpIleGIlnGIuThrMetIysAsnAsn 230
Db 944 GACTGATCCAGAGACGATGAAGAACAT 973
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AAV84589 standard; DNA; 1146 BP.
ID AAV84589
AC XX
XX AAV84589;
DT 01-MAR-1999 (first entry)
XX
XX Human secreted protein gene 179 clone HETBX14.
XX
XX Human: secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclasts; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
XX W09854963-A2.
PN
XX 10-DEC-1998.
PD
XX 04-JUN-1998; 98WO-US11422.
PF
XX 18-DEC-1997; 97US-0070923.
PR 06-JUN-1997; 97US-0048877.
PR 06-JUN-1997; 97US-0048881.

PR 06-JUN-1997; 97US-0048884.
PR 06-JUN-1997; 97US-0048893.
PR 06-JUN-1997; 97US-0048896.
PR 06-JUN-1997; 97US-0048899.
PR 06-JUN-1997; 97US-0048915.
PR 06-JUN-1997; 97US-0048949.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048972.
PR 06-JUN-1997; 97US-0049020.
PR 06-JUN-1997; 97US-0049375.
PR 05-SEP-1997; 97US-0057628.
PR 05-SEP-1997; 97US-0057635.
PR 05-SEP-1997; 97US-0057644.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057661.
PR 05-SEP-1997; 97US-0057667.
PR 05-SEP-1997; 97US-0057761.
PR 05-SEP-1997; 97US-0057764.
PR 05-SEP-1997; 97US-0057770.
PR 05-SEP-1997; 97US-0057775.
PR 05-SEP-1997; 97US-0057778.
PR 06-JUN-1997; 97US-0048875.
PR 06-JUN-1997; 97US-0048878.
PR 06-JUN-1997; 97US-0048882.
PR 06-JUN-1997; 97US-0048885.
PR 06-JUN-1997; 97US-0048894.
PR 06-JUN-1997; 97US-0048897.
PR 06-JUN-1997; 97US-0048900.
PR 06-JUN-1997; 97US-0048916.
PR 06-JUN-1997; 97US-0048962.
PR 06-JUN-1997; 97US-0048970.
PR 06-JUN-1997; 97US-0048974.
PR 06-JUN-1997; 97US-0049373.
PR 05-SEP-1997; 97US-0057584.
PR 05-SEP-1997; 97US-0057625.
PR 05-SEP-1997; 97US-0057642.
PR 05-SEP-1997; 97US-0057645.
PR 05-SEP-1997; 97US-0057648.
PR 05-SEP-1997; 97US-0057651.
PR 05-SEP-1997; 97US-0057662.
PR 05-SEP-1997; 97US-0057668.
PR 05-SEP-1997; 97US-0057762.
PR 05-SEP-1997; 97US-0057765.
PR 05-SEP-1997; 97US-0057771.
PR 05-SEP-1997; 97US-0057776.
PR 06-JUN-1997; 97US-0048876.
PR 06-JUN-1997; 97US-0048880.
PR 06-JUN-1997; 97US-0048883.
PR 06-JUN-1997; 97US-0048892.
PR 06-JUN-1997; 97US-0048895.
PR 06-JUN-1997; 97US-0048898.
PR 06-JUN-1997; 97US-0048901.
PR 06-JUN-1997; 97US-0048917.
PR 06-JUN-1997; 97US-0048963.
PR 06-JUN-1997; 97US-0048971.
PR 06-JUN-1997; 97US-0049019.
PR 05-SEP-1997; 97US-0049374.
PR 05-SEP-1997; 97US-0057627.
PR 05-SEP-1997; 97US-0057634.
PR 05-SEP-1997; 97US-0057643.
PR 05-SEP-1997; 97US-0057646.
PR 05-SEP-1997; 97US-0057654.
PR 05-SEP-1997; 97US-0057666.
PR 05-SEP-1997; 97US-0057760.
PR 05-SEP-1997; 97US-0057763.
PR 05-SEP-1997; 97US-0057769.
PR 05-SEP-1997; 97US-0057774.
PR 05-SEP-1997; 97US-0057777.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX

PI Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA;
PI Fan P, Feng P, Ferrie AM, Fischer CL, Florence C;
PI Florence K, Greene JM, Hu J, Kyaw H, Lafleur DM;
PI Li Y, Moore PA, Ni Y, Olsen HS, Rosen CA, Ruben SM;
PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
XX
DR WPI: 1999-059865/05.
DR P-PSDB: AAM88712, AAM89041, AAM89042, AAM89043.
XX
XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 4: Page 441-442: 772pp: English.
XX
XX The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
CC encoding human secreted proteins (AAM88534 to AAM88756). The secreted
CC protein gene sequences are deposited with the ATCC under deposit numbers
CC ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
CC cells comprising recombinant vectors containing the nucleic acid
CC sequences are used for the recombinant production of the secreted
CC proteins. The polynucleotide and amino acid sequences are useful for are
CC useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pathological conditions can be also
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the polynucleotides, based on
CC which tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC restenosis, prostate diseases, obesity, disorders involving osteoclasts
CC such as osteoporosis, arthritis or malignancies, diseases of testes,
CC lung or thymus, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.
CC The present sequence represents a gene encoding a human secreted protein
CC (see descriptor line for gene number and clone identification).
XX
XX Sequence 1146 BP: 282 A; 347 C; 272 G; 237 T; 8 other;
SO
Alignment Scores:
Pred. No: 1.39e-104 Length: 1146
Score: 1253.00 Matches: 228
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 2
Query Match: 99.21% Indels: 0
DB: 20 Gaps: 0

US-09-856-320A-2_COPY_53_282 (1-230) x AAV84589 (1-1146)

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DB 121 AGGATCATCAAGGGGTTGAGTGCAGGCTCAGTCCAGCCCTGCGAGGAGCCCTGTTC 180
QY 21 GlutylthraaleuLeuCyGlyAlaThrleulealaProaqtgtrpleuLeuThrala 40
DB 181 GAGAAAGCGCGCTACTCTGTGGGGCGAGCGTCAATCGCCCAATGCTCTTACACCA 240
QY 41 AlahiscysleuLysProaqtgtrileValhislleuglylnhlsasnleuGlnLysGlu 60
DB 241 GCCCAGTCCCTCAAGCCCGCTACATAGTTCACCTGGGGAGCACAACCTCCAGAGAG 300
QY 61 GluInlyGysGluGlnThrArgThralaThrcLusSerPheprohlsproGlyPheasn 80
DB 301 GAGGAGCTGTGGACAGCCCGGACGCCATGATCTTCCGCCACCCGCGCTTCAACCAAC 360
QY 81 SerleuproasnLysAspHisAlaArgasnAspIlelleuValLysMetAlaSerProval 100
DB 361 AGCCTCCCAACAAAGACACCGCAATGACATCATGCTGTGAAGATGGCATGCCAGTC 420

QY 101 SerIlethrTPalalaValArgProleuThrLeuSerSerArgCysValThralaGlyThr 120
DB 421 TCCATCACCCTGGGCTGTGCGACCCCTCCTCTCCAGCTGTGTCACGTGGGACCC 480
QY 121 SerCysleuIleSerGlyTrnglySerThrSerSerProGlnleuArgLeuProhlsThr 140
DB 481 AGCTGCTCATATTTCCGGCTGGGGCGAGMACGTCACACCCCGATTAAGCGCTGCTCACACC 540
QY 141 LeuArgCysAlaAsnIleThrIleleGlnhlsGlnLysCysGluAsnAlaTyProGly 160
DB 541 TTGSATCCGCCACATCATCATCATTTAGACACCGAAGTGTGAGAACGCTACCCCGCC 600
QY 161 AsnIlethrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
DB 601 AACATCACAGACACCATGTTGTGTGCCAGCTGCAGAAAGGGGCGAAGACTCTGCCAG 660
QY 181 GlyAspSerGlyGlyProleuValCysasnGlnSerleuGlnGlyIleIleSerTrpGly 200
DB 661 GGTGACTCTGGGGGCGCCCTGTGTGTAACAGTCTTCAAGCGCATTAATCTCTGGGGC 720
QY 201 GlnAspProCysAlaIleThrArgLysProGlyValTyThrLysValCysLysTyVal 220
DB 721 CAGATCTCGTGTGCGATCACCCGAAAGCTGTGTCTACACGMAAGTGTCAATATGTG 780
QY 221 AspTrpIleGlnGluThrMetLysAsn 230
DB 781 GACTGATCCAGAGACGATGAGAACAT 810
XX
XX RESULT 15
XX ABA83430
XX ID ABA83430 standard; cDNA; 1146 BP.
XX
XX ABA83430:
XX
XX 07-FEB-2002 (first entry)
XX
XX Human secreted protein gene 179 SEQ ID NO:247.
XX
XX DE
XX
XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
XX dermatological; immunosuppressive; antiinflammatory; immunostimulant;
XX cytosstatic; cardiant; vascular; anti-angiogenic; ophthalmological;
XX neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnery;
XX antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
XX multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
XX human immunodeficiency virus; hyperproliferative disorder; wound healing;
XX Chagar's cardiomyopathy; coronary arteriosclerosis; angiogetic disorder;
XX corneal graft neovascularisation; diabetic retinopathy; regeneration;
XX neurological disorder; Huntington's chorea; Alzheimer's disease;
XX Parkinson's disease; infectious disease; ss.
XX
XX OS Homo sapiens.
XX
XX NCBI accession: W0200162891-A2.
XX
XX PD 30-AUG-2001.
XX
XX
XX 21-FEB-2001: 2001WO-US05614.
XX
XX 24-FEB-2000: 2000US-184836P.
XX
XX 29-MAR-2000: 2000US-193170P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX NI J, Ebner R, Lafleur DM, Moore PA, Olsen HS, Rosen CA;
XX Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
XX Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;
XX Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
XX Zeng Z, Greene JM;
XX
XX WPI: 2001-625724/72.
XX DR P-PSDB: ABB50537.
XX

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 23, 2002, 14:17:42 ; Search time 36 Seconds

(without alignments)
187,980 Million cell updates/sec

Title: US-09-856-320A-2_COPY_53_282

Perfect score: 1263
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1232	97.5	248	4	US-08-944-483-24
3	1221.5	96.7	289	4	US-09-386-642-14
4	686	54.3	260	3	US-09-025-059-3
5	683	54.1	260	3	US-09-070-526-2
6	675	53.4	260	4	US-09-008-271A-7
7	673.5	53.3	288	4	US-09-386-642-13
8	597.5	47.3	268	2	US-08-824-874-1
9	587.5	47.3	268	4	US-08-210-084-1
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12	596.5	47.2	263	3	US-08-807-151-5
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17	582.5	46.1	244	3	US-08-767-820A-10
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24	582.5	46.1	261	4	US-08-983-075D-7
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27	579.5	45.9	261	3	US-08-767-820A-19

28	579.5	45.9	261	3	US-08-622-046B-3	Sequence 3, Appl1
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30	579	45.8	247	2	US-08-956-267A-2	Sequence 2, Appl1
31	578.5	45.8	244	5	PCT-US95-06157-10	Sequence 10, Appl1
32	578.5	45.8	261	5	PCT-US95-06157-6	Sequence 6, Appl1
33	578	45.8	237	2	US-08-978-404B-45	Sequence 45, Appl1
34	577.5	45.7	237	3	US-08-768-859A-16	Sequence 16, Appl1
35	577.5	45.7	237	3	US-08-767-820A-16	Sequence 16, Appl1
36	577.5	45.7	237	3	US-08-622-046B-12	Sequence 12, Appl1
37	577.5	45.7	237	4	US-08-944-483-37	Sequence 37, Appl1
38	577.5	45.7	238	3	US-09-100-264-1	Sequence 1, Appl1
39	577.5	45.7	238	3	US-08-768-859A-8	Sequence 8, Appl1
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42	577	45.7	228	1	US-08-483-859-7	Sequence 7, Appl1
43	577	45.7	228	1	US-08-472-173-7	Sequence 7, Appl1
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45	577	45.7	228	2	US-08-482-816-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-025-059-1
Sequence 1, Application US/09025059
Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Nell C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTU10
CLONE: 2723646
US-09-025-059-1
Query Match 100.0%; Score 1263; DB 3; Length 282;
Best Local Similarity 100.0%; Pred. No. 2, 3e-126;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIIFGECRPHSQPQWQALFEKTRLLCGATLTPRMLTFAHCLKPRYIVHIGOHNLQKE 60
DB 53 RIIFGECRPHSQPQWQALFEKTRLLCGATLTPRMLTFAHCLKPRYIVHIGOHNLQKE 112
QY 61 EGCQRTATSEFPHPGFNSLPKNDHRNDIMLVKMASPVSTWAVRPLTSSRCVTAGT 120
DB 113 EGCQRTATSEFPHPGFNSLPKNDHRNDIMLVKMASPVSTWAVRPLTSSRCVTAGT 172
QY 121 SCLISGSGTSSPOLRPLPHTLRCAANTITIEHOKCENAYPGNITDYMVCASVOEGGKDSQ 180
DB 173 SCLISGSGTSSPOLRPLPHTLRCAANTITIEHOKCENAYPGNITDYMVCASVOEGGKDSQ 232
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DB 233 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 282

RESULT 2
US-08-944-483-24
; Sequence 24, Application US/08944483
; Patent No. 6232456

GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,483
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: NO. 62324566
US-08-944-483-24

Query Match 97.5%; Score 1232; DB 4; Length 248;

Best Local Similarity 99.1%; Pred. No. 3.7e-123;
Matches 228; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 RIIFGECRPHSQPQWQALFEKTRLLCGATLTPRMLTFAHCLKPRYIVHIGOHNLQKE 60
DB 21 RIIFGECRPHSQPQWQALFEKTRLLCGATLTPRMLTFAHCLKPRYIVHIGOHNLQKE 78
QY 61 EGCQRTATSEFPHPGFNSLPKNDHRNDIMLVKMASPVSTWAVRPLTSSRCVTAGT 120
DB 79 EGCQRTATSEFPHPGFNSLPKNDHRNDIMLVKMASPVSTWAVRPLTSSRCVTAGT 138
QY 121 SCLISGSGTSSPOLRPLPHTLRCAANTITIEHOKCENAYPGNITDYMVCASVOEGGKDSQ 180
DB 139 SCLISGSGTSSPOLRPLPHTLRCAANTITIEHOKCENAYPGNITDYMVCASVOEGGKDSQ 198
QY 181 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 230
DB 199 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 248

RESULT 3
US-09-386-642-14
; Sequence 14, Application US/09386642
; Patent No. 6420157

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew
APPLICANT: OL, Jensen
APPLICANT: Andrade-Gordon, Patricia

TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642

CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Fusion gene

OTHER INFORMATION: With homo sapien serine protease catalytic domain
US-09-386-642-14

Query Match 96.7%; Score 1221.5; DB 4; Length 289;

Best Local Similarity 96.5%; Pred. No. 6.1e-122;
Matches 223; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 RIIFGECRPHSQPQWQALFEKTRLLCGATLTPRMLTFAHCLKPRYIVHIGOHNLQKE 59
DB 51 RIIFGECRPHSQPQWQALFEKTRLLCGATLTPRMLTFAHCLKPRYIVHIGOHNLQKE 110

QY 60 EGCQRTATSEFPHPGFNSLPKNDHRNDIMLVKMASPVSTWAVRPLTSSRCVTAGT 119
DB 111 EGCQRTATSEFPHPGFNSLPKNDHRNDIMLVKMASPVSTWAVRPLTSSRCVTAGT 170

QY 120 TSCGISGSGTSSPOLRPLPHTLRCAANTITIEHOKCENAYPGNITDYMVCASVOEGGKDSQ 179
DB 171 TSCGISGSGTSSPOLRPLPHTLRCAANTITIEHOKCENAYPGNITDYMVCASVOEGGKDSQ 230

QY 180 QDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 230
DB 231 QDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 281

RESULT 4
US-09-025-059-3
; Sequence 3, Application US/09025059
; Patent No. 6075136

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.

TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE


```

:
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESS: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Dr.
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/025,059
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PR-0481 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 260 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: Genbank
: CLONE: 1020091
: US-09-025-059-3

Query Match          54.3%; Score 686; DB 3; Length 260;
Best Local Similarity 52.8%; Pred. No. 4,66-65;
Matches 121; Conservative 36; Mismatches 70; Indels 2; Gaps 2;

QY 1 RIIGFECKPHSOPQWALFEKTRLLCGATLIAPRMILTAHCKLPRIYVHGOHNLQKE 60
DB 32 KILRGECIPHSOPQWALFEGERLICGVLVGDWVLTAAHCKKQKYSVRLGDHSLSR 91
QY 61 EGCEQTRATESFPHPGNNSLPNKDHNDIMLVKMASPVSIITAVRPLTSSRCVTAGT 120
DB 92 DQPEGEIVVQSIHPPCVNNNSP-EDHSHDMLRLQNSANLGDVKFVQOLANLCPKVGQ 150
QY 121 SCLISGWSTSSPOLRLPHTRCANITIEHOKCENAYPGNITDTMVCASVOEGGKDSQ 180
DB 151 KCIISGWTIVSPQENFNTINCAEVRKIYSQNKCEKATPGKITEGMVAG-SSNADPTCQ 209
QY 181 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTRKVKYVDMIOETMKN 229
DB 210 GDSGGLVNCNOSLOGIISWGSDPCGKPKKPGVYTRKVKYVDMIOETMKN 258

RESULT 5
US-09-070-526-2
: Sequence 2, Application US/09070526
: GENERAL INFORMATION:
: APPLICANT: SOUTHAN, CHRISTOPHER
: APPLICANT: CLINKENBEARD, HELEN
: APPLICANT: BURGESS, NICOLA
: TITLE OF INVENTION: No. 6100059e1 Compounds
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: RATNER & PRESTIA
: STREET: P.O. BOX 980
```

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:
: CITY: VALLEY FORGE
: STATE: PA
: COUNTRY: USA
: ZIP: 19482
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/070,526
: FILING DATE: 30-APR-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9711952.3
: FILING DATE: 9-JUN-1997
: APPLICATION NUMBER: EP 97309646.4
: FILING DATE: 1-DEC-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: PRESTIA, PAUL F
: REGISTRATION NUMBER: 23,031
: REFERENCE/DOCKET NUMBER: GH-30353
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-407-0700
: TELEFAX: 610-407-0701
: TELEX: 846169
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 260 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-070-526-2

Query Match          54.1%; Score 683; DB 3; Length 260;
Best Local Similarity 51.6%; Pred. No. 9,66-65;
Matches 116; Conservative 43; Mismatches 64; Indels 2; Gaps 2;

QY 1 RIIGFECKPHSOPQWALFEKTRLLCGATLIAPRMILTAHCKLPRIYVHGOHNLQKE 60
DB 32 KVLGGECQPHSOPQWALFEQGLCGVLVGGWVLTAAHCKKPKTYVRIGDHSLSQNK 91
QY 61 EGCEQTRATESFPHPGNNSLPNKDHNDIMLVKMASPVSIITAVRPLTSSRCVTAGT 120
DB 92 DQPEGEIVVQSIHPPCVNNNS-DVEDHNDMLRLQROASIGSKVRKISLADHCTQPGQ 150
QY 121 SCLISGWSTSSPOLRLPHTRCANITIEHOKCENAYPGNITDTMVCASVOEGGKDSQ 180
DB 151 KCIISGWTIVSPQENFNTINCAEVRKIYPQKCEDAYPGOITDGMVCASSSKA-DTCQ 209
QY 181 GDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTRKVKYVDMIOE 225
DB 210 GDSGGLVNCNOSLOGIISWGSDPCGKPKKPGVYTRKVKYVDMIOE 254

RESULT 6
US-09-008-271A-7
: Sequence 7, Application US/09008271A
: Patent No. 6203979
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: Hillman, Jennifer L.
: Guegler, Karl J.
: Corley, Neil C.
: Tang, Tom Y.
: Shan, Purvi
: TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Dr.
```


Best Local Similarity 49.18; Pred. No. 1.2e-55;
Matches 110; Conservative 39; Mismatches 68; Indels 7; Gaps 4

[illegible]

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RESULT 9
US-09-210-084-1
Sequence 1, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
type: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANOT02
CLONE: 820694
US-09-210-084-1

```

Query Match	47.3%	Score 597.5;	DB 4:	Length 268;
Best Local Similarity	49.18	% Pred. No. 1,2e-55;		
Matches 110;	Conservative 39;	Mismatches 68;	Indels 7;	Gaps 4;
OY	8 CKPSQWQAALFEKTRILCGATLAPRWLLTAACHLKPRIVVHIGQNLIK-EEGCEOT	66		
	50 CTP-SRQAAALLLPNDLCAGAVLVHPDMLTAAHCRRKVRVRVGRGHSLSPVYSGGOM	108		

Oy	67	RTAIESPFHPENNSLPKHKDRNDIMLYKMASPVSITMAVPEPLTSLSCVTAGSCLISG	128
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	109	FQGVASIDPHPSY----HPSGSNDLMILMKIRRIAPRTKDVAIPNVASHCPDAGTKCLVSG	164
Oy	127	WGTS ^{SS} POLRLPHLTRCANITIEHOKCENAYPGNINDTWCAVSOGGRKSCGGDSGGP	186
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	165	WGTIKSPVHPFKYLQCINISVLSQKRCEBAYPMQIDDTMFCAG-DKAGRSDCGDGGGP	223
Oy	187	LVCNCSLOGITSMGDCPCAIRRKGAVTYKVKCYVDIMIOEPMKNK	230
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	224	VYCKGSLDGLYSKWDYPCPARNRNGVYTNNLCKFTKMTAQIETIQAN	267

```

RESULT 10
US-08-790-137-4
Sequence 4, Application US/08790137
Patent No. 5840871
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Suyu K.
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
TITLE OF INVENTION: KALLIKREIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,137
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0195 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 55527
US-08-790-137-4

```

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Query Match          47.2%  Score 596.5:  DB 2:  Length 263:
 .Best Local Similarity 44.8%  Pred. No.1,5e-55:
Matches 107;  Conservative 44;  Mismatches 79;  Indels 9;  Gaps 2

OY  1  RIRIGGECKPISOPQALAEFKTRLLCGATLLAPRWLLTAALCKAPRYIVHGGHMLAKE 60
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db  24  RIRIGGFCEKKSQPHVAVYRFAHQCGGVLLDANWVLAALCYANDKYQVWGLKNNRFED 83
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

OY  61  EGCEQRTATSFPPHPGFNNSLPNKDH-----RNDIMLVKMASPVSIITAVAPRLTLES 112
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db  84  EPSAOHQLISAIIPHPGNNMSLLNDDHDPHPEDDYSNDIMLVKRPAPITTVVKKRIDLP 143
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

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QY 113 SRCVATGSCILISMGWST-SPOLRLPTTLACATITIEHOKCNAPGNTDTPWASV 171
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 144 TEEPTVGSRCILASMGWSTTPEEFYSHDQCYLELISNVCYKAKTEKTYDMLCAGE 203
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 QEGKDSQGSNGSGRPVYCNOSLQITISMGDPCATIKRPGYTYTVYVCYVIMDETAKNN 230
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 204 MDGGADTICVGSNGGLIDGVLYQITISMGPPCLPVPNGLYITKLILRYSMIKYKVMANN 262
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 11
 US-08-824-874-5
 Sequence 5, Application US/08824874
 Patent No. 5962300
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Lal, Preeti
 TITLE OF INVENTION: NOVEL KALLIKREIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/824,874
 FILING DATE: Filed Herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0252 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 263 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Genbank
 CLONE: 55527
 US-08-824-874-5

Query Match	47.2%	Score 596.5	DB 2	Length 263
Best Local Similarity	44.8%	Pred. 1.5e-55		
Matches 107	Conservative 44	Mismatches 79	Indels 9	Gaps 2

QY	1	RIRGFECKPSPQWQALFEKTRLCATYLIAPWLLTAHCLKPRYIVHGHNLQKE	60
		::: ::: ::: ::: ::: ::: ::: :::	
Db	24	RIRGFENCKSPQHPVAVVPAPRQCGVLLDANWVLTAAACYNDKXQVWGLKNRRFED	83
		::: ::: ::: ::: ::: ::: :::	
QY	61	EGCEQTRTATSPFPHGNNSLPNKDH-----RNDIMETKASPSYITWVRPLTUS	112
		::: ::: ::: ::: ::: ::: :::	
Db	84	EPSAQHOLISKAIRPHPGNMSLLNDRHPREDYSNDLMLRLKPPAETIDVVRIDLP	143
		::: ::: ::: ::: ::: ::: :::	
QY	113	SRCTAGAGSCILISGGGTS-SPOLRLPHTLRICANTTIIHOKECENAYCGNTIDWVCASV	171
		::: ::: ::: ::: ::: ::: :::	
Db	144	TEETPTSGRLASGNGSTTPTTEEFYSHDLCVYIELLSNEVCANAEKTVDTMLCAEE	203
		::: ::: ::: ::: ::: ::: :::	
QY	172	QEGKSDSCGGSDGPLYVGNOSLGLIISGODPCATIRKPGVYTKVCKVDMIQETMRKN	230
		::: ::: ::: ::: ::: ::: :::	

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[illegible]

```

: Sequence 5, Application US/09210084
: Patent No. 6197511
:
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Lal, Preeti
: TITLE OF INVENTION: NOVEL KALLIKREIN
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/210,084
: FILING DATE:
:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/824,874
: FILING DATE:
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0252 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 263 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: Genbank
: CLONE: 55527
:
: US-09-210-084-5

```

RESULT 14
US-09-478-957-5
Sequence 5, Application US/09478957
Patent No. 6350448
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: lal, Preeti
TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED

TITLE OF INVENTION: PROTEASE
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: US
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/478,957
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/807,151
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0227 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 263 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Genbank
 CLONE: 55527
 IS-09-478-957-5

RESULT 15
 US-08-978-404B-44
 ; Sequence 44, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; TITLE OF INVENTION: FIBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston

STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5968782e
US-08-978-404B-44

Query Match 46.6%; Score 589; DB 2; Length 246;
Best Local Similarity 48.3%; Pred. No. 8.8e-55;
Matches 11; Conservative 35; Mismatches 78; Indels 6; Gaps 3;

QY 1 RIITGFECRPHSOPWQALPEKTRILGATLIPRWLFTAHCILKPRYIVHIGOHNLQKE 60
DB 23 KIVGTYICPEHSVPYQVSL-NSGYHFCGSLINDQWVSAHCKSKRIQVRLGEHNINVL 81
QY 61 EGCEQRTATESPPHPGFNNSLPNKDRNDIMLVKASPVSYTMAVRPLTLSSRCYTAGT 120
DB 82 EGDEQFINAKIKIHPYSSWTLN---NDIMLIKLSPPVKINARVAPALPSACAPAGT 137
QY 121 SCLISGWGTSSTSPQLRPLPHLRKANITIIIEHCKENAYPGNITDTMYCASVQEGKDSQ 180
DB 138 QCLISGWGNTLSNGVNNPDLQCDAPVLSQADCEAAYPGEITSSMICVGFLEGGKDSQ 197
QY 181 GDSGCPLYCNOSLOGITISWGQDPCATRRKRPVYTKVCKYVDWIOETMKNN 230
DB 198 GDSGGPVVCMGQLGIVSMGIY-CALPDNPGVYTKVCGNFGWIODTIAAN 246

Search completed: December 23, 2002, 14:23:33
Job time : 37 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 23, 2002, 14:22:47 ; Search time 3129 Seconds

(without alignments)
2139.228 Million cell updates/sec

Title: US-09-856-320A-2_COPY_53_282

Perfect score: 1263
Sequence: 1 RIITGFECKPHSQPMQALF.....GYTCKVCKYDWIQTWKN 230

Scoring table:

BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPRO.spool/US09856320/runat.23122002.113711.22694/app.query.fasta.1.391
-DB=GenEmbl -GFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USBR=US09856320.@CGN.1.1.3637.@runat.23122002.113711.22694 -NCPV=6 -ICPV=3
-NO_XLPPY -NO_MMAR -LARGOUBRY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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27: em_sts:*
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29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
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34: em_htg_pln:*
35: em_htg_rtd:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
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41: em_htgo_other:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	1263	100.0	1106	6 AX016287	AX016287 Sequence
2	1263	100.0	1158	6 AX016289	AX016289 Sequence
3	1263	100.0	1181	9 AB013730	AB013730 Homo sapi
4	1263	100.0	1186	9 AB012917	AB012917 Homo sapi
5	1263	100.0	1192	6 AR152174	AR152174 Sequence
6	1263	100.0	1204	6 AX358932	AX358932 Sequence
7	1263	100.0	1204	6 AX362425	AX362425 Sequence
8	1263	100.0	1204	6 AX454622	AX454622 Sequence
9	1263	100.0	1204	6 AX464372	AX464372 Sequence
10	1263	100.0	1204	6 AX491100	AX491100 Sequence
11	1263	100.0	1213	6 BC022068	BC022068 Homo sapi
12	1263	100.0	1301	6 AB041036	AB041036 Homo sapi
13	1263	100.0	1314	6 AR098430	AR098430 Sequence
14	1251	99.0	1166	6 AR152173	AR152173 Sequence
15	1218	96.4	833	6 AR060847	AR060847 Sequence
16	1067	84.5	1213	10 AB016226	AB016226 Mus muscu
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18	961	76.1	9120	9 AF164623	AF164623 Homo sapi
19	961	76.1	132323	9 AC011473	AC011473 Homo sapi
20	961	76.1	230000	9 AF243527	AF243527 Homo sapi
21	948	75.1	142334	2 AC073185	AC073185 Homo sapi
22	902.5	71.5	201797	2 AC130782	AC130782 Pan trogl
23	890.5	70.5	178609	2 AC130188	AC130188 Papio cyn
24	689	54.6	974	10 RRA5641	RAJ005641 Rattus ra
25	686	54.3	1322	6 AX305781	AX305781 Sequence
26	686	54.3	1322	10 MUSNEU	D30785 Mouse mRNA
27	686	54.3	1333	6 E12348	E12348 cDNA encodi
28	684	54.2	963	6 AX360075	AX360075 Sequence
29	684	54.2	1278	6 AX46461	AX46461 Sequence
30	683	54.1	868	6 E32037	E32037 human neuro
31	683	54.1	868	9 AB009849	AB009849 Homo sapi
32	683	54.1	905	6 E28146	E28146 Novel serin
33	683	54.1	905	6 E40546	E40546 Novel serin
34	683	54.1	905	6 AB008390	AB008390 Homo sapi
35	683	54.1	942	6 E28147	E28147 Novel serin
36	683	54.1	942	6 E40547	E40547 Novel serin
37	683	54.1	944	6 AX002035	AX002035 Sequence
38	683	54.1	944	6 E31440	E31440 Novel compo
39	683	54.1	998	6 AB008927	AB008927 Homo sapi
40	683	54.1	999	6 AX080795	AX080795 Sequence
41	683	54.1	999	6 AX454486	AX454486 Sequence
42	683	54.1	999	6 AX464262	AX464262 Sequence
43	683	54.1	999	6 AX480964	AX480964 Sequence
44	683	54.1	1007	9 AF095742	AF095742 Homo sapi
45	683	54.1	1360	9 AF055982	AF055982 Homo sapi

RESULT 1

ALIGNMENTS

AX016287
LOCUS AX016287 1106 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from Patent WO949055.
ACCESSION AX016287
VERSION AX016287.1 GI:10041854
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.
TITLE Human casb12 polypeptide, a serine protease
JOURNAL Patent: WO 949055-A 1 30-SEP-1999;
BRUCK CLAUDE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);
COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
(BE)
FEATURES
source location/Qualifiers
BASE COUNT 247 a 348 c 287 g 224 t
ORIGIN
Alignment Scores:
Pred. No.: 2.24e-97 Length: 1106
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-856-320A-2_COPY_53_282 (1-230) x AX016287 (1-1106)
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DB 170 AGATCTCAAGGGGTTTCGAGTGCAGCCCTCACCAGCCCTGGGAGGAGCCCTGTC 229
21 GlulysThrArgleuleucysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 40
|||||
DB 230 GAGAGACGGGGCTACTGTGGGGGAGGAGCTCATGCCCCAGATGGCTCTGACAGCA 289
41 AlaHisCysleuysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnysGlu 60
|||||
DB 290 GCCCAGCTCTCAAGCCCGCTACATAGTTCACCTGGGGAGACAACTCCAGAAAGAG 349
61 GlulGlyCysGlnGlnThrArgTrpAlaThrGluSerPheProHisProGlyPheAsn 80
|||||
DB 350 GAGGCTGTGAGCAGACCCGAGACAGCAGTCCCTCCGCCACCCCGGCTTCACACAC 409
81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
|||||
DB 410 AGCTCTCCCAACAAAGACCCGCAATGACATGCTGTGTAAGATGGATCGCCAGTC 469
101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
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DB 470 TCCATACCTGGGCTGTGGCAGCCCTCACCTCTCTCCACAGCTGTGTCACTGTGGCACC 529
121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
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DB 530 AGTGGCTCTATTCCGGGCTGGGAGACAGCTCCAGCCCGAGTTAGCGCTGCTCACACC 589
141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGly 160
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DB 590 TTGCGATGGCCCAACATACACATCATTTGAGCAGACAGAGTGTAGAAAGCGCTACCCGGC 649
161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
|||||
DB 650 AACATACAGACACATGTTGTGTGTCAGGCTGACAGAAAGGCGCAAGCTCTCCAGC 709
181 GlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlnIleIleSerTrpGly 200
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DB 710 GGTGACTCCGGGGGCGCTCTGGTCTGTACCAAGTCTCTTCAGAGCATTTCTCTGGGGC 769

QY 201 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrVal 220
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DB 770 CAGATCCCGTGTGGATCACACCCGAAAGCCGTGTGTACACGAAAGTCTGCAATATGTC 829
QY 221 AspTrpIleGlnGlnLuthrMetLysAsnAsn 230
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DB 830 GACTGATCCAGAGACGATGAAGAACAAAT 859
RESULT 2
LOCUS AX016289 1158 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 3 from Patent WO949055.
ACCESSION AX016289
VERSION AX016289.1 GI:10041855
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.
TITLE Human casb12 polypeptide, a serine protease
JOURNAL Patent: WO 949055-A 3 30-SEP-1999;
BRUCK CLAUDE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);
COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
(BE)
FEATURES
source location/Qualifiers
BASE COUNT 274 a 359 c 306 g 219 t
ORIGIN
Alignment Scores:
Pred. No.: 2.35e-97 Length: 1158
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-856-320A-2_COPY_53_282 (1-230) x AX016289 (1-1158)
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DB 240 AGATCTCAAGGGGTTTCGAGTGCAGCCCTCACCAGCCCTGGGAGGAGCCCTGTC 299
21 GlulysThrArgleuleucysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 40
|||||
DB 300 GAGAGACGGGGCTACTGTGGGGGAGGAGCTCATGCCCCAGATGGCTCTGACAGCA 359
41 AlaHisCysleuysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnysGlu 60
|||||
DB 360 GCCCAGCTCTCAAGCCCGCTACATAGTTCACCTGGGGAGACAACTCCAGAAAGAG 419
61 GlulGlyCysGlnGlnThrArgTrpAlaThrGluSerPheProHisProGlyPheAsn 80
|||||
DB 420 GAGGCTGTGAGCAGACCCGAGACAGCAGTCCCTCCGCCACCCCGGCTTCACACAC 479
81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
|||||
DB 480 AGCTCTCCCAACAAAGACCCGCAATGACATGCTGTGTAAGATGGATCGCCAGTC 539
101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
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DB 540 TCCATACCTGGGCTGTGGACCCCTCACCTCTCTCCACAGCTGTGTCACTGTGGCACC 599
121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
|||||
DB 600 AGTGGCTCTATTCCGGGCTGGGAGACAGCTCCAGCCCGAGTTAGCGCTGCTCACACC 659
141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGly 160


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Db 660 TTGGGATGCGCCACATACCATTCATTGAGCACCAGAAAGTGTGAGAACGCTACCCGCGC 719
Oy 161 Asn1IhrasprhmetvalcysalaserValGIngluglylylsaspsercysgln 180
Db 720 AACATCAGACACACCATGCTGTGTGCGAGCGTGCAGGAAGGGGCGAAGACTCTCGGCGAG 779
Oy 181 glyaspserglyglyproleuValcysansgInserleugInglylleIleSerTrpGly 200
Db 780 GGTGACTCCGGGGGCGCCCTGCTGTGTACACAGCTCTTCAAGGCATATCTCTCGGGCG 839
Oy 201 GlnaspproCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
Db 840 CAGATCGCTGTGCGATCACCAGAAAGCTGTGTACAGAAAGTCTGCATAATATGTG 899
Oy 221 AsprTrpIleGIngluThrMetLysAsnAsn 230
Db 900 GACTGATCCAGAGACGATGAAGAACAT 929

RESULT 3
AB013730 1181 bp mRNA linear PRI 20-JUN-2000
LOCUS Homo sapiens mRNA for Hippostasin, complete cds.
DEFINITION AB013730.1 GI:6681453
VERSION AB013730.1 GI:6681453
KEYWORDS Hippostasin.
SOURCE Homo sapiens Hippocampus and Prostate cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Mitsui,S., Yamada,T., Okui,A., Komimami,K., Uemura,H. and
Yamaguchi,N.
TITLE A novel isoform of a kallikrein-like protease, TLSP/hippostasin,
(JRMS20), is expressed in the human brain and prostate
Biochem. Biophys. Res. Commun. 272 (1), 205-211 (2000)
20329229
2 (bases 1 to 1181)
Yamaguchi,N. and Mitsui,S.
REFERENCE Direct Submission
JOURNAL Submitted (08-MAY-1998) Nozomi Yamaguchi, Kyoto Prefectural
University of Medicine, Res. Ins. Geriatrics; Kawarimachi Hirokoji,
Kyoto, Kyoto 602-8566, Japan (E-mail:nozomi@koto.kpu-m.ac.jp,
Tel:81-75-251-5848, Fax:81-75-251-5848)
FEATURES
source location/Qualifiers
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/db_xref="taxon:9606"
/lisue_type="Hippocampus and Prostate"
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/translation="MRLQLILALATGLVGETRIIKGECKPSPQWALFEKTR
LLCGATLIAPRWLITAHCKPRYIVLGHNLIKKEGCEQITAESEFHPFNNSL
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Best Local Similarity: 100.00% Mismatches: 0
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DB: 9
US-09-856-320a-2_COPY_53_282 (1-230) x AB013730 (1-1181)

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102b
 102b

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1. .1186
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/db_xref="taxon:9606"
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CDS
/codon_start=1
/product="serine protease (TLSP)"
/protein_id="BAA3404.1"
/db_xref="GI:3649791"
/translation="MORLRMLRDMKSSGGRLTAKEPGARSPLOAMRILOLILALA
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HIGOHNLCKEECEQRTAPESPSPHGFNNSLPNKMRNDIMLYKASVSTWNR
LTLSSRCTVAGTSCILSGWSTSSPOLRPHILDKANITIIIEOKENAPGNTIDTM
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/product="TLSP"
polya_signal 1164. .1169
polya_site 1186
/note="12 a nucleotides"
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Alignment Scores:
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Score: 1263.00 Matches: 230
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x AB012917 (1-1186)

QY 1 ArgIlellelelysglypnehiucyslyspProHisSerGlnProTrpGlnAlaLeuPhe 20
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QY 21 GluLysThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 40
|||||
Db 242 GAGAGACGCGGGCTACTCTGTGGGGCGACGCTATCGCCCCAGATGGCTCTGACAGCA 301
QY 41 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
|||||
Db 302 GCCCAGCTGCTCAAGCCCGCTCAATAGTTCACCTGGGGCAGCAACCTCCAGAAAGAG 361
QY 61 GluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 80
|||||
Db 362 GAGGGGTGTGAGCAGACCCGAGCAGCCACAGTCCCTCCACCACCCGGCTTCAACAC 421
QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
|||||
Db 422 AGCTCCCCCAACAAAGACCCGCAATGACATCATGCTGTGAGATGGCATGCGCAGTC 481
QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
|||||
Db 482 TCCATCACCTGGGCTGTGGACCCCTCACCTCTCTCCACAGCTGTGTACCTGTGGCACC 541
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
|||||
Db 542 AGTGGCTCATTTCCGGCTGGGGGAGACAGCTCCAGCCCCAGTTAGCCCTGCTCACACC 601
QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTrpProGly 160
|||||
Db 602 TTGCGATGGCGCCAAATCATCATATTGACACACAGAAAGTGAGAAAGCGCTACCCGGC 661
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180
|||||
Db 662 AACATACACACACATCATGTGTGTGCGAGGTCCAGAAAGGGGCAAGGACTCTCCAGAG 721
QY 181 GlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
|||||
Db 722 GGTGACTCCGGGGGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 781

QY 201 GlnAspProCysAlaIleThrArgLysProGlyValIleTrpThrLysValCysLysTrpVal 220
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Db 782 GAGATCCGCTGTGCGATCACCCGAAAGCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 841
QY 221 AspTrpIleGlnGluThrMetLysAsnAsn 230
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Db 842 GACTGATCCAGAGAGAGATGAAGAACAAT 871

RESULT 5
AR152174
LOCUS AR152174 1192 bp DNA linear PART 08-AUG-2001
DEFINITION Sequence 8 from patent US 6232456.
ACCESSION AR152174
VERSION AR152174.1 GI:15118224
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 1192)
Cohen,M., Colpitts,T.L., Friedman,P.N., Granados,E., Kias,M.R.,
AUTHORS Russell,J.C., Stewart,K.D. and Stroupe,S.D.
TITLE Serine protease reagents and methods useful for detecting and
treating diseases of the prostate
JOURNAL Patent: US 6232456-A 8 15-MAY-2001;
FEATURES Location/Qualifiers
source 1. .1192
BASE COUNT 279 a 385 c 290 g 238 t
ORIGIN

Alignment Scores:
Pred. No.: 2.43e-97 Length: 1192
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x AR152174 (1-1192)

QY 1 ArgIlellelelysglypnehiucyslyspProHisSerGlnProTrpGlnAlaLeuPhe 20
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QY 21 GluLysThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 40
|||||
Db 227 GAGAGACGCGGGCTACTCTGTGGGGGAGGAGCTATGCCCCAGATGGCTCTGACAGCA 286
QY 41 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
|||||
Db 287 GCCCAGCTGCTCAAGCCCGCTCAATAGTTCACCTGGGGCAGCAACCTCCAGAAAGAG 346
QY 61 GluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 80
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Db 347 GAGGGCTGTGAGCAGACCCGAGCAGCCACTGACTCTTCCCCACCCCGCTTCAACAC 406
QY 81 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 100
|||||
Db 407 AGCTCCCCCAACAAAGACCCGCAATGACATCATGCTGTGAGATGGCATGCGCAGTC 466
QY 101 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 120
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Db 467 TCCATCACCTGGGCTGTGGACCCCTCACCTCTCTCCACAGCTGTGTACCTGTGGCACC 526
QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 140
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Db 527 AGTGGCTCATTTCCGGCTGGGGGAGACAGCTCCAGCCCCAGTTAGCCCTGCTCACACC 586
QY 141 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTrpProGly 160
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Db 587 TTGCGATGGCGCCAAATCATCATATTGACACACAGAAAGTGAGAAAGCGCTTACCCGGC 646
QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 180

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Db 647 AACATCAGACAGACCATGCTGTGTGCCAGCTGCAGAAAGGGGGGCAAGCATCTCTGCCAG 706
QY 181 GYASPERGIGLYPProLeuValCYASnGInSerLeuGInGlyIleIleSerTriGly 200
Db 707 GGTACACTCCGGGGGCGCTCTGTGTGTGTACCAAGCTCTTCAAGGCATTATCTCTGGGGC 766
QY 201 GInAspProCYsAlaIleHrArGLysProGlyValTyrThrLYsValCYsLYsTyrVal 220
Db 767 CAGATCCGTTGGTGGATCACCCGAAAGCTGTGTCTACAGAAAGTGTGCAATATGTG 826
QY 221 AsPTrPIleGInGluThrMetLYsAsn 230
Db 827 GACTGATCCAGAGACGATGAACAAT 856

RESULT 6
AX358932 1204 bp DNA linear PAT 13-FEB-2002
LOCUS Sequence 185 from Patent WO0193983.
ACCESSION AX358932
VERSION AX358932.1 GI:18675367
KEYWORDS
SOURCE
ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Baker,K.P., Desnoyers,L., Gerltsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smth,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0193983-A 185 13-DEC-2001;
JOURNAL Genentech Inc. (US)
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN

Alignment Scores:
Pred. No.: 2.45e-97 Length: 1204
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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VERSION AX362425.1 GI:18694670
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Baker,K.P., Desnoyers,L., Gerltsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smth,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0208288-A 185 31-JAN-2002;
JOURNAL Genentech, Inc. (US)
FEATURES
source location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN

Alignment Scores:
Pred. No.: 2.45e-97 Length: 1204
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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VERSION	AX454622.1																																									
KEYWORDS	GI:21713935																																									
SOURCE	human.																																									
ORGANISM	Homo sapiens																																									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																																									
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.																																									
TITLE	1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,																																									
JOURNAL	Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,																																									
	Pan,J.N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.																																									
	and Ye,W																																									
	Compositions and methods for the diagnosis and treatment of																																									
	disorders involving anglogenesis																																									
	Patent: WO 0208284-A 207 31-JAN-2002;																																									
	Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone																																									
	(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,																																									
	Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;																																									

Percent Similarity:	100.00%	Conservative:	0
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DB 226 GAGAAAGACCGCGCTACTGTGGGGGAGAGCTCATATCGCCCCAGATGGCTCTGACAGA 285			
QY 41 AlaHisCysLeuLysProArgTrpIleValHisIleGluGlnHisAsnLeuGlnLysGlu 60			
DB 286 GCCCACTGGCTCAAGCCCGCTACATAGTCACTCCGGGGACACAAACCTCCAGAGAG 345			
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DEFINITION Sequence 505 from Patent WO0140466.			
ACCESSION AX464372			
VERSION AX464372.1 GI:21899202			
KEYWORDS human.			
SOURCE Homo sapiens			
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE 1 Baker,K.P., Bersini,L.M., DeForge,L., Desnoyers,L., Filvaroff,E., Geo,W.O., Gerlitsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Wetanabe,C.K., Wood,W.L. and Zhang,Z.			
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same			

JOURNAL		Patent: WO 0140466-A 505 07-JUN-2001;	
Genentech Inc. (US)			
FEATURES	Location/Qualifiers		
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Score:	1263.00	Matches:	230
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QY	41	AlaHlsCysLeuLysProArgTyrTrlLevalHlsleuGlyGlnHlsAsnleuGlnLysGlu	60
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QY	61	GluclycysgluGlnThrArgThrAlaThrGluSerPheProHlsProGlyPheAsnAsn	80
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DEFINITION	Sequence 207 from Patent WO0200690.		linear
ACCESSION	AX491100.1		
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KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
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REFERENCE	1			
AUTHORS	Baker, K.P., Ferrar, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsden, S.A., Pan, J., Pooni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.			
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis			
JOURNAL	Patent: WO 0200690-A 207 03-JAN-2002;			
FEATURES	Genentech, Inc. (US)			
source	location/Qualifiers			
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BASE COUNT	306 a	364 c	294 g	240 t
ORIGIN				
Alignment Scores:				
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Percent Similarity:	100.00%	Conservative:	0	
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QY	81	SerleuProAsnLysAspHisArgAsnAspIleMetleuValLysMetAlaSerProval	100	
Db	406	AGCCTCCCCACAAAGACACCGCAATGACATCATGCTGGGAAGATGGATGCCAGTC	465	
QY	101	SerIlethrTPAlaValArgProleuthrIleuSerSerArgCysValIThrAlaGlyThr	120	
Db	466	TCCATCACCTGGGTGGCGACCCCTCACCTCTCCACAGCTGTCTCACCTGTGCACC	525	
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QY 221 AsptPrilEgInglunhrMetLysAsn 230
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RESULT 11
BC022068

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complete cds.

ACCESSION BC022068
VERSION BC022068.1 GI:18314497

KEYWORDS MGC.

SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1213)

REFERENCE 1
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapsb-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Heltton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

FEATURES
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location/Qualifiers
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CDS
376 c 296 g 251 t

BASE COUNT 290 a 376 c 296 g 251 t

ORIGIN

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Pred. No.: 2,47e-97 Length: 1213
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-856-320a-2_COPY_53_282 (1-230) x BC022068 (1-1213)

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Db 793 CAGGATCCGCTGCTGATGACCCGAAAGCCGCTGTCTACAGAAAGTGTCAATATGTG 852

QY 221 AsptPrilEgInglunhrMetLysAsn 230
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Db 853 GACTGATCCAGACGATGAACAAT 882

RESULT 12
AB041036

LOCUS AB041036 1301 bp mRNA linear PRI 20-JUN-2000
DEFINITION Homo sapiens mRNA for prostate-type 11prostaticin, complete cds.
ACCESSION AB041036
VERSION AB041036.1 GI:8574438
KEYWORDS prostate-type 11prostaticin.
SOURCE Homo sapiens prostate cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (sites)

REFERENCE 1
AUTHORS Mitsui, S., Yamada, T., Okui, A., Koninami, K., Uemura, H. and
Yamaguchi, N.
TITLE A novel isoform of a kallikrein-like protease, TLSP/11prostaticin,
JOURNAL (PKSS20), is expressed in the human brain and prostate
MEDLINE Biochem. Biophys. Res. Commun. 272 (1), 205-211 (2000)
20329229
REFERENCE 2 (bases 1 to 1301)
AUTHORS Yamaguchi, N. and Mitsui, S.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2000) Nozomi Yamaguchi, Kyoto Prefectural

University of Medicine, Res. Ins. Geriatrics, Kawamachi Hirokoji,
Kyoto, Kyoto 602-8566, Japan (E-mail: nozomilekoto.kpu-m.ac.jp,
Tel: 81-75-251-5848, Fax: 81-75-251-5848)

FEATURES

source

1. 1301

/organism="Homo sapiens"

/db.xref="taxon:9606"

/tissue="prostate"

113. 961

/codon_start=1

/product="prostate-type histoplasin"

/protein_id="AA96797.1"

/db.xref="GI:8574439"

/translation="MQRRLRMKSSGRGLTAKEPGANSSPLQALRIQLITLALA
TGLVGEETRIIKFECKPHSQPQWALFEKRLGATLAPRWLLPAHCKEPRIV
HLGQHNLOKEGGEQPTATESPFPENRDMIVKASPSITVAWRP
LTLSRCVATGSLISMGSTSPQRLPITLCAITTIIEHCKENAVPGNTIDM
VCASVQSGKSDSCGDSGSPVLCNOSLOGIISWQDPCALTRKGVYTRKCYDWIG
EPMKNN"

CDS

BASE COUNT 332 a 387 c 330 g 252 t
ORIGIN

Alignment Scores:

Pred. No.: 2,67e-97 Length: 1301
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x AB041036 (1-1301)

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DB 269 AGGATCATCAAGGGGTGAGTGCAGAGCCCTCCAGCCCTGGCAGGAGCCCTGTC 328
QY 21 GlutysprraargleuleucysglyalathrleuilealaproaagtprleuLeuthrAla 40
DB 329 GAGAAAGACGGCGTACTGTGGGGCGAGCTCATCGCCCGCAGATGGCTCTGCACACA 388
QY 41 Alaniscysleuysproargtyrillevalhlsleuglylnhlsanleuglnlysglu 60
DB 389 GCCCATCTCCTCAAGCCCGCTACCTACCTACCTGCGGCGACACACCTCCAGAGAG 448
QY 61 GlutylcysgluglnthrArgThrAlathrgluserrpheprohissproglypheasn 80
DB 449 GAGGGCTGTGACAGACCCGGAGACCCACTGAGTCTCCCGCCAGCCCGGCTTCAACAC 508
QY 81 SerleuproasnlysaasphisaargasnasprilemetleuValysmetAlaserProva 100
DB 509 AGCTCCCAACAAAGACACCGGACATGATGCTGTGAAGATGGCATCGCCAGTC 568
QY 101 SerleuproasnlysaasphisaargasnasprilemetleuValysmetAlaserProva 120
DB 569 TCCATACACCTGGGCTGTGGAGCCCTCCCTCTCTACCTGTGTACCTGTGTGTG 628
QY 121 SerlysleuileserglytprglyserthrserserProglinleuargleuprohisThr 140
DB 629 AGCTGCCCATTTCCGGCTGGGGAGCAGCTCCAGCCCGCAGTTACGCTCTCCACAC 688
QY 141 LeuargcysAlaasnillethrilleelguhlsGlnlyscysgluasnAlaTyProgly 160
DB 689 TTGGGATGGCCCAACATCATCATTTAGCACAGAAAGTGTGAAGAGCGCTACCCGGC 748
QY 161 AsnillethraaprrhmetValaCysAlaserValglnluglylylsaspserscysgln 180
DB 749 AACATCAACAGACACCATCATCATTTAGCACAGAAAGTGTGAAGAGCGCTACCCGGC 808
QY 181 GlyspsersglylyproleuValaCysanglnserleuglnlylleIsertprgly 200
DB 809 GGTACTCCGGGGGCGCTCTGTGTGAACAGTCTTCAAGGACATATATCTCTGGGGC 868
QY 201 GlnasproCysAlailethraArglyspProglyValTyThrlyValCyslystTyVal 220

DB 869 CAGGATCCGTGTGGCATACCCGAAAGCCTGGTGTCTACAGAAAGTGTGCAAAATATGTG 928
QY 221 AsprtrpIleglnluThrMetlysaasn 230
DB 929 GACTGTGATCCAGACCATGATGAAGACAAT 958

RESULT 13

LOCUS AR098430 1314 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6075136.
ACCESSION AR098430
VERSION AR098430.1 GI:12807687

KEYWORDS

Unknown.

ORGANISM Unknown.

REFERENCE

1 (bases 1 to 1314)
Tang, Y.Tom., Corley, N.C. and Guejler, K.J.
Prostate-associated serine protease
Patent: US 6075136-A 2 13-JUN-2000;
Location/Qualifiers

FEATURES

source 1. 1314

BASE COUNT 320 a 400 c 337 g 257 t
ORIGIN

Alignment Scores:

Pred. No.: 2.7e-97 Length: 1314
Score: 1263.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320a-2_COPY_53_282 (1-230) x AR098430 (1-1314)

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QY 21 GlutysprraargleuleucysglyalathrleuilealaproaagtprleuLeuthrAla 40
DB 344 GAGAAAGACGGCGTACTGTGGGGCGAGCTCATCGCCCGCAGATGGCTCTGCACACA 403
QY 41 Alaniscysleuysproargtyrillevalhlsleuglylnhlsanleuglnlysglu 60
DB 404 GCCCATCTCCTCAAGCCCGCTACCTACCTACCTGCGGCGACACACCTCCAGAGAG 463
QY 61 GlutylcysgluglnthrArgThrAlathrgluserrpheprohissproglypheasn 80
DB 464 GAGGGCTGTGACAGACCCGGAGACCCACTGAGTCTCCCGCCAGCCCGGCTTCAACAC 523
QY 81 SerleuproasnlysaasphisaargasnasprilemetleuValysmetAlaserProva 100
DB 524 AGCTCCCAACAAAGACACCGGACATGATGCTGTGAAGATGGCATCGCCAGTC 583
QY 101 SerleuproasnlysaasphisaargasnasprilemetleuValysmetAlaserProva 120
DB 584 TCCATACACCTGGGCTGTGGAGCCCTCCCTCTCTACCTGTGTACCTGTGTGTG 643
QY 121 SerlysleuileserglytprglyserthrserserProglinleuargleuprohisThr 140
DB 644 AGCTGCCCATTTCCGGCTGGGGAGCAGCTCCAGCCCGCAGTTACGCTCTCCACAC 703
QY 141 LeuargcysAlaasnillethrilleelguhlsGlnlyscysgluasnAlaTyProgly 160
DB 704 TTGGGATGGCCCAACATCATCATTTAGCACAGAAAGTGTGAAGAGCGCTACCCGGC 763
QY 161 AsnillethraaprrhmetValaCysAlaserValglnluglylylsaspserscysgln 180
DB 764 AACATCAACAGACACCATCATCATTTAGCACAGAAAGTGTGAAGAGCGCTACCCGGC 823

OY	181	GATGACCTCGGGGGCCCTTGTGTTGAACAAGTCCTTAAGGCATTATCCTCGGCC		883
OY	201	ClnaspproCysAlaIleThrArgLysProGlyValTYrThrLysValCysLysTyraI		220
Db	884	CAGATACCGTGTCGCAATCCGAAAGCCTGTGTCTACAGAAGTGTGCAAATATGTG		943
OY	221	AspTPRIeGLingluThrmetylsnasn	230	
Db	944	GACTGTATCCAGAGAACATGAAGAAT	973	
RESULT 14				
LOCUS	ARI52173		1166 bp	DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 7 from patent US 6232456.			
ACCSSION	ARI52173			
VERSION	ARI52173.1	GI:15118223		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1166) Cohen,M., Colpitts,T.L., Friedman,P.N., Granados,E., Klaas,M.R., Russell,J.C., Stewart,K.D. and Strome,S.D. Serine protease reagents and methods useful for detecting and treating diseases of the prostate Patent: US 6232456-A 7 15-MAY-2001; Location/Qualifiers 1..1166 . /organism="unknown"			
JOURNAL FEATURES	source			
BASE COUNT	259 a	381 c	285 g	237 t 4 others
ORIGIN				
Alignment Scores:				
Pred. No.:	2.43e-96	Length:	1166	
Score:	1251.00	Matches:	228	
Percent Similarity:	99.13%	Conservative:	0	
Best Local Similarity:	99.13%	Mismatches:	2	
Query Match:	99.05%	Indels:	0	
DB:	6	Gaps:	0	
US-09-856-320A-2_COPY_53_282 (1-230) x ARI52173 (1-1166)				
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Db	163	AGGATCATCAAGAGGGGTTGAGTGCNAGGCTCACCTCCAGCCTGCGACAGCACCTGTTC		222
OY	21	GluystrArqzleuleucygsalyalathrlleulielaiproatgrTrpleueuthrla		40
Db	223	RAGARACGGGCTVACTGTGGGGGAGAGCCTCAATCGCCCCAGTAGTGCTCTCGACAGCA		282
OY	41	AlahisCyLeulyaProArgtyrtilevalHIsleaugLYgmHisAsmleuglmynsglu		60
Db	283	GGCCACTGCGCTCAAGCCCCTGACTAATGTtaccctgggagacacacactccagaaggag		342
OY	61	GluglyCySGluclnThrArgThrallathrgluserrpheprohisproglypheasnasn		80
Db	343	GAGGGCTGTGAGACAGCCCGGAGACCCACTGAGTCTTCCCCACCCGGCTTCAACAAAC		402
OY	81	SerleupProashlysAspHisArgasnsapliekelleuVallysMetalaserProyal		100
Db	403	AGCCCTCCCAACAAAAGACACCGCAATGACATCAATGATGATGATAATGATGATGATG		462
OY	101	SerllethrTPPalavalArgProleuthrhleuserratargcyvalThralaglythr		120
Db	463	TCCATCACCTGGGCTGTGGAGCCCTCACCTCTCTCAAGCGTGTGTACTGTGTCGACAC		522
OY	121	SercysleuIliseseglyTYrpolyserThrseserProginleuaArgleuprohisThr		140
Db	523	AGCTGCTCATTTTCGGGTGGGGGAGCAACGTGCACCCGCCAGTTTACGGCTGCTCACACC		582
OY	141	LeuatgcysAliaasnillethrllleledunhsiglinlyscysgluasnalatryrProgly		160

[illegible]


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QY 121 SerCysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThr 140
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Db 456 AGTGCCCTCATTTCCGGCTGGGCGACGTCACGCCCTTACGCTGCTCACACC 515
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QY 141 LeuArgCysAlaAsnIleThrIleIleGlnIleLysCysGluAsnAlaTyrProGly 160
    |||
Db 516 TTGGGATGGCCAAATCACCATTGAGCACGAGAGTGTGAGAAAGCCTACCCGCGC 575
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QY 161 AsnIleThrAspThrMetValCysAlaSerValGlnGlyIleLysAspSerCysGln 180
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Db 576 AACATCACAGACACCATGTGTGTGCCAGCGTCGACGAGAGGGGCAAGGACTCCTGCCAG 635
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QY 181 GlyAspSerGlyIleProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 200
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Db 636 GGTGACTCCGGGGGCCCTCTGTGTAAACAGTCTTCAAGGCATTATCTCTGGGGC 695
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QY 201 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 220
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Db 696 CAGGATCCGTGTCCGATCACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAAAATATGTG 755
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QY 221 AspTrpIleGlnIleThrMetLysAsnAsn 230
    |||
Db 756 GACTGGATCCAGAGACGATGAGAGACAAAT 785
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Search completed: December 23, 2002, 16:02:33
Job time : 3136 secs

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; Sequence 284, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (185)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (201)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-898-284
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Query Match 56.9%; Score 719; DB 10; Length 247;
Best Local Similarity 57.2%; Pred. No. 3.6e-59;
Matches 131; Conservative 33; Mismatches 65; Indels 0; Gaps 0;
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Db 19 RAIGAECCRNQSPWQAGLHRLTFCGATLISDRWLLTAHCKLPRIYVHLCQHNLOKE 78
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QY 61 ECGEQTTRATESPFPNNSLPKNDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGT 120
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Db 79 EGPEQLFRVTDFFPHPEFNKDLANDHNDIMLRPRQARLSAVOPLNLSQTCVSPGM 138
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QY 121 SCLISGSGTSSPOLRLPHRLRCANITIIHOKCENAYPGNITDTWCASVQSGKDSQC 180
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Db 139 QCLISGSGXSSPKALPFPVTLQCANISILENKLCMAVPHGISDSMXCAGLMEGGRSCQ 198
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QY 181 GDSGGLPVCNOSLOGIISMGODPCATIRKPGVYTKVCKYVDWIOETMKN 229
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Db 199 GDXGGLPVCNGLAGVVGGAEPGSRPRRAVYTSVCHYLDWIOELMEN 247
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RESULT 3
US-09-764-847-742
; Sequence 742, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 742
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (148)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (185)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (201)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-847-742
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Query Match 56.9%; Score 719; DB 10; Length 247;
Best Local Similarity 57.2%; Pred. No. 3.6e-59;
Matches 131; Conservative 33; Mismatches 65; Indels 0; Gaps 0;
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QY 1 RIIGFECRHSOPWQALAEKTRLLCGATLLAPRWLLTAHCKLPRIYVHLCQHNLOKE 60
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Db 19 RAIGAECCRNQSPWQAGLHRLTFCGATLISDRWLLTAHCKLPRIYVHLCQHNLOKE 78
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 61 ECGEQTTRATESPFPNNSLPKNDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGT 120
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 79 EGPEQLFRVTDFFPHPEFNKDLANDHNDIMLRPRQARLSAVOPLNLSQTCVSPGM 138
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 121 SCLISGSGTSSPOLRLPHRLRCANITIIHOKCENAYPGNITDTWCASVQSGKDSQC 180
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 139 QCLISGSGXSSPKALPFPVTLQCANISILENKLCMAVPHGISDSMXCAGLMEGGRSCQ 198
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 181 GDSGGLPVCNOSLOGIISMGODPCATIRKPGVYTKVCKYVDWIOETMKN 229
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 199 GDXGGLPVCNGLAGVVGGAEPGSRPRRAVYTSVCHYLDWIOELMEN 247
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```
RESULT 4
US-09-796-294-8
; Sequence 8, Application US/09796294
; Patent No. US20020037581A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Extracellular Serine Protease
; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 8
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of mouse neutropilin homologous
; OTHER INFORMATION: to TAD0-14; accession no. D30785
; US-09-796-294-8
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Query Match 54.3%; Score 686; DB 10; Length 260;
Best Local Similarity 52.8%; Pred. No. 4.3e-59;
Matches 121; Conservative 36; Mismatches 70; Indels 2; Gaps 2;
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QY 1 RIIGFECRHSOPWQALAEKTRLLCGATLLAPRWLLTAHCKLPRIYVHLCQHNLOKE 60
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 32 KILGREGCIPIHSQPMQALPQGERLGGVLDVDRVLTAAHCKKQYSVRLDHLQSR 91
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 61 ECGEQTTRATESPFPNNSLPKNDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGT 120
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
Db 92 DPEOEIOVNOASTIOHPCYNSNP-EDHSHDILIRLQNSANLKDCKYQVQIANLCPKVGQ 150
   |||:|||||: |||:|||||: |||:|||||: |||:|||||: |||:|||||:
QY 121 SCLISGSGTSSPOLRLPHRLRCANITIIHOKCENAYPGNITDTWCASVQSGKDSQC 180
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Db 151 KCIISGCTVTSPOENFNPNTLNCFAEVKITSQNCERATPGKITBGMVACG-SSNGADTCQ 209
QY 181 GDSGGLVNCNSLOGIISWGDPCATRRPGVYTKVKCYVDMIQETMRN 229
Db 210 GDSGGLVCDGMLGQITSMGSDPGCKRPEKPGVYTKVICHYITWIKTKTMN 258

RESULT 5
US-09-888-615-90
; Sequence 90, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHITE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARVYZAK, GLEN
; APPLICANT: MANNING, GERRARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888, 615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214, 047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-90

Query Match 54.2%; Score 684; DB 10; Length 320;
Best Local Similarity 51.7%; Pred. No. 8.4e-56;
Matches 124; Conservative 37; Mismatches 65; Indels 14; Gaps 3;

QY 1 RIINGECKPSOPWQAALFEKTRLLCGATLIAPRMLITAAHCKLPRIYVHLGCHNLQKE 60
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QY 61 EGCQOTRATSEFPHPGNNLSLPKNDHNDIMLYKMASPVSTIYAVRPLTSSRCVYAGT 120
Db 145 DGPDLRTTSVYIPHPRE---ARSHRNDIMLRVQPARLNPQVRAVLPTRCPHPGE 200
QY 121 SCLISGWCSTSP-----SP--QLRLPHTLRCANITIEHOKENAYPGNITDMVCAS 170
Db 201 ACVYSGMCLVSHNRPGRAGSPRSQVSLPDTLHCANISITISDCKSTPGKRLNIMVACG 260
QY 171 VOEGGKDCQCGDSGGLVNCNSLOGIISWGDPCATRRPGVYTKVKCYVDMIQETMRN 230
Db 261 AEGRGAECEGDSGGLVNCNSLOGIISWGDVPCDNTTKPGVYTKVCHYLEMIMETMRN 320

RESULT 6
US-09-978-295A-395
; Sequence 395, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
```

```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978, 295A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 54.1%; Score 683; DB 9; Length 260;
Best Local Similarity 51.6%; Pred. No. Re-56;
Matches 116; Conservative 43; Mismatches 64; Indels 2; Gaps 2;

QY 1 RIHKFECRHSQPMQALFEKTRLLCGATLIPRWILTRAHLKPRYIHLGONHIOKE 60
DB 32 KVLGHECOPHSQPMQALFEKTRLLCGATLIPRWILTRAHLKPRYIHLGONHIOKE 91
QY 61 EGCEQRTATESPFPHPENSLPNKDHNDIMLVKMASPVSTWAVRPLTSSRCVTAGT 120
DB 92 DPEQDELIVVQSLPHFCYNS-DVEDHNDIMLVKMASPVSTWAVRPLTSSRCVTAGT 150
QY 121 SCLISGSGTSPQLRPLHTRLCANITIEHOKCENAYPENGITDTWVCAVQEGGRDSCQ 180
DB 151 KCTVSGMGVTSPRENPDPTLNCAYKIFQKCEADAYPEQITDGMVCAVQEGGRDSCQ 209
QY 181 GDSGGLVCDGALOGITSMGSDPCGRSDKFGVYTNICRYLDMWIKK 225
DB 210 GDSGGLVCDGALOGITSMGSDPCGRSDKFGVYTNICRYLDMWIKK 254

RESULT 7
US-09-978-697-395
Sequence 395, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT FILING DATE: 2001-10-16
CURRENT FILING DATE: 2001-09-27, 697
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Query Match 54.1%; Score 683; DB 9; Length 260;
Best Local Similarity 51.6%; Fred. No. 8e-56;
Matches 116; Conservative 43; Mismatches 64; Indels 2; Gaps 2;

QY 1 RIIFGFEKPSHPWQALFEKFLCGATLIPRMILTAHCLKPRYIVHLGOHNLQXE 60
Db 32 KVLGHEHCQHSQPMQALFQGOQLGVLGVGNWVLTAAHCKKRYTRLGSHLQNK 91
QY 61 EGCQRTATSPPHGPFNNLSLPKDRNDIMLVKMASPVSTWAVRPLTSSKCVTACT 120
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Db 151 KCVVSGGVTSPRENPDILNCAEYVIFPOKCEDAYPQOITDGVCASSGKA-DTQC 209
QY 181 GDSGGPLVCNQLGITSWGDDPCATRRKPGVTKVKCYDWIOE 225
Db 210 GDSGGPLVCALOGITISWGSDDPCGSKDGPVYTNINICRYLDWIKK 254

RESULT 8
US-09-978-192A-395
Sequence 395, Application US/09978192A
Patent No. US2002017753A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 1998-07-09

Query Match Best Local Similarity 51.4%; Score 649.5; DB 9; Length 293;
Matches 118; Conservative 40; Mismatches 67; Indels 7; Gaps 4;

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Db 66 RINSGDCDMHTQPMQALLRPNOLYCGAVYHQPWILTAAHCKKFRRLGHTSIP 125
Oy 60 -EEGCEQTRTATESPHEGFNNSLPNKDRNDIMLVKNASPVSTMAVRPLTSSRCVYA 118
Db 126 VYESQGMFOGKKSIPHGYS---HPGHSNDLMLIKINRRIRPKDYRPIVSSHCPSA 181
Oy 119 GTSCLSGMSSTSSPQLPHTLRCAANTTIEHCKCEANAYGNITDVMWCAVQSGKDS 178
Db 182 GTKCLVSGWGTTPSPVHPFVYLQCLNTSVLSQKCEADAYPPQIDDTMFCAG-DIAGHDS 240
Oy 179 CGDSSGCPVLCVNSLOGILISMGQDPCATRRKGVYTKYCKYDWMIOETMKN 230
Db 241 CGDSGGFVVCNGLSLQGLVSMGDYFCARNRGGVTTNCKFTKWIOETIOAN 292

US-09-989-293A-309
Sequence 309, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonl, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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RESULT 14
US-09-989-722-309
Sequence 309, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
PRIOR FILING DATE: 2001-11-19
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 51.4%; Score 649.5; DB 10; Length 293;

Best Local Similarity 50.9%; Pred. No. 1,1e-52; Mismatches 67; Indels 7; Gaps 4;

Matches 118; Conservative 40; Mismatches 67; Indels 7; Gaps 4;

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DB 66 RIIRGSDCDHPTQWQAALLLRPMQLYCAVLVHPQMLTAAHCRKRVFRRLGHYSLSLSP 125
QY 60 -EECCQTRATBSFPHGKNSLPMKDNNDMLVMASPVSTTAAVRPLTSSRCVTA 118
DB 126 VYEGSQMFGQVKSIPHGYS---HGHSNDLMLIKLRIRIPTKDVPRINSSHCPSA 181
QY 119 GTSLGSGWSTSPQRLHTLRCANITIIIEHOKCENAVPGNTTDMVCAVQEGGKDS 178
DB 182 GTKCLVSGWGTTSPOVHFPRVLCILNISVLSQRCEADATPRQIDIDTDFCAG-DKAGRDS 240

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RESULT 15
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Sequence 309, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT FILING DATE: 2001-11-19
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      PRIOR FILING DATE: 1998-07-09

Query Match: 51.4%; Score 649.5; DB 10; Length 293;
Best Local Similarity 50.9%; Pred. No. 1,1e-52;
Matches 118; Conservative 40; Mismatches 67; Indels 7; Gaps 4;

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